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(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract

Novel polynucleotides and the proteins encoded thereby are disclosed.

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SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 126 to nucleotide 485;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 207 to nucleotide 485;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb2_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb2_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 126 to nucleotide 485; the nucleotide sequence of SEQ ID NO:1 from nucleotide 207 to nucleotide 485; the nucleotide sequence of the full-length protein coding sequence of clone vb2_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vb2_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(bb) the nucleotide sequence of the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 126 to nucleotide 485, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 126 to nucleotide 485, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 126 to nucleotide 485. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 207 to nucleotide 485, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 207 to nucleotide 485, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 207 to nucleotide 485.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 130 to nucleotide 2286;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 214 to nucleotide 2286;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb3_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb3_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 130 to nucleotide 2286; the nucleotide sequence of SEQ ID NO:3 from nucleotide 214 to nucleotide 2286; the nucleotide sequence of the full-length protein coding sequence of clone vb3_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vb3_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 354 to amino acid 363 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 130 to nucleotide 2286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 130 to nucleotide 2286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 130 to nucleotide 2286. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 214 to nucleotide 2286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from

nucleotide 214 to nucleotide 2286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 214 to nucleotide 2286.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 354 to amino acid 363 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 172 to nucleotide 522;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 214 to nucleotide 522;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb4_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb4_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 172 to nucleotide 522; the nucleotide sequence of SEQ ID NO:5 from nucleotide 214 to nucleotide 522; the nucleotide sequence of the full-length protein coding sequence of clone vb4_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vb4_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 172 to nucleotide 522, and extending

contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 172 to nucleotide 522, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 172 to nucleotide 522. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 214 to nucleotide 522, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 214 to nucleotide 522, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 214 to nucleotide 522.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 119 to nucleotide 502;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 176 to nucleotide 502;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb5_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb5_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 119 to nucleotide 502; the nucleotide sequence of SEQ ID NO:7 from nucleotide 176 to nucleotide 502; the nucleotide sequence of the full-length protein coding sequence of clone vb5_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vb5_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(bb) the nucleotide sequence of the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 119 to nucleotide 502, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 119 to nucleotide 502, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 119 to nucleotide 502. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 176 to nucleotide 502, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 176 to nucleotide 502, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 176 to nucleotide 502.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 128 to nucleotide 436;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 203 to nucleotide 436;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb6_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb6_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 128 to nucleotide 436; the nucleotide sequence of SEQ ID NO:9 from nucleotide 203 to nucleotide 436; the nucleotide sequence of the full-length protein coding sequence of clone vb6_1 deposited under accession number ATCC 98804; or the

nucleotide sequence of a mature protein coding sequence of clone vb6_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 128 to nucleotide 436, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 128 to nucleotide 436, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 128 to nucleotide 436. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 203 to nucleotide 436, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 203 to nucleotide 436, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 203 to nucleotide 436.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 138 to nucleotide 1250;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 279 to nucleotide 1250;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb7_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb7_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 138 to nucleotide 1250; the nucleotide sequence of SEQ ID NO:11 from nucleotide 279 to nucleotide 1250; the nucleotide sequence of the full-length protein coding sequence of clone vb7_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vb7_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 180 to amino acid 189 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 138 to nucleotide 1250, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 138 to nucleotide 1250, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 138 to nucleotide 1250. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 279 to nucleotide 1250, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 279 to nucleotide 1250, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 279 to nucleotide 1250.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 180 to amino acid 189 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 615 to nucleotide 869;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb8_1 deposited under accession number ATCC 98804;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb8_1 deposited under accession number ATCC 98804;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 615 to nucleotide 869; the nucleotide sequence of the full-length protein coding sequence of clone vb8_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vb8_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(ab) the nucleotide sequence of the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 615 to nucleotide 869, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 615 to nucleotide 869, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 615 to nucleotide 869.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 1470;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 193 to nucleotide 1470;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb9_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb9_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 1470; the nucleotide sequence of SEQ ID NO:15 from nucleotide 193 to nucleotide 1470; the nucleotide sequence of the full-length protein coding sequence of clone vb9_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vb9_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3′ end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3′ end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15 , but excluding the poly(A) tail at the 3′ end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 1470, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 1470, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide

148 to nucleotide 1470. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 193 to nucleotide 1470, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 193 to nucleotide 1470, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 193 to nucleotide 1470.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 109 to nucleotide 414;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 217 to nucleotide 414;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc3_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc3_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 109 to nucleotide 414; the nucleotide sequence of SEQ ID NO:17 from nucleotide 217 to nucleotide 414; the nucleotide sequence of the full-length protein coding sequence of clone vc3_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc3_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the

fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ab) the nucleotide sequence of the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(bb) the nucleotide sequence of the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 109 to nucleotide 414, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 109 to nucleotide 414, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 109 to nucleotide 414. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 217 to nucleotide 414, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 217 to nucleotide 414, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 217 to nucleotide 414.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 169 to nucleotide 840;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 211 to nucleotide 840;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc4_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc4_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 169 to nucleotide 840; the nucleotide sequence of SEQ ID NO:19 from nucleotide 211 to nucleotide 840; the nucleotide sequence of the full-length protein coding sequence of clone vc4_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc4_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide

encodes the full-length or a mature protein encoded by the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 169 to nucleotide 840, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 169 to nucleotide 840, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 169 to nucleotide 840. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 211 to nucleotide 840, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 211 to nucleotide 840, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 211 to nucleotide 840.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 508 to nucleotide 951;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 733 to nucleotide 951;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc5_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc5_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 508 to nucleotide 951; the nucleotide sequence of SEQ ID NO:21 from nucleotide 733 to nucleotide 951; the nucleotide sequence of the full-length protein coding sequence of clone vc5_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc5_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(ab) the nucleotide sequence of the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 508 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 508 to nucleotide 951, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 508 to nucleotide 951. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 733 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 733 to nucleotide 951, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 733 to nucleotide 951.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 125 to nucleotide 493;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc7_1 deposited under accession number ATCC 98748;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc7_1 deposited under accession number ATCC 98748;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 125 to nucleotide 493; the nucleotide sequence of the full-length protein coding sequence of clone vc7_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc7_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 125 to nucleotide 493, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 125 to nucleotide 493, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 125 to nucleotide 493.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 33 to nucleotide 407;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 99 to nucleotide 407;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc9_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc9_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 33 to nucleotide 407; the nucleotide sequence of SEQ ID NO:25 from nucleotide 99 to nucleotide 407; the nucleotide sequence of the full-length protein coding sequence of clone vc9_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc9_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(ab) the nucleotide sequence of the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(bb) the nucleotide sequence of the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 33 to nucleotide 407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 33 to nucleotide 407, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 33 to nucleotide 407. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 99 to nucleotide 407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from

nucleotide 99 to nucleotide 407, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 99 to nucleotide 407.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 176 to nucleotide 871;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc10_1 deposited under accession number ATCC 98748;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc10_1 deposited under accession number ATCC 98748;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 176 to nucleotide 871; the nucleotide sequence of the full-length protein coding sequence of clone vc10_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc10_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 176 to nucleotide 871, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 176 to nucleotide 871, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 176 to nucleotide 871.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 160 to nucleotide 657;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 214 to nucleotide 657;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc11_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc11_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 160 to nucleotide 657; the nucleotide sequence of SEQ ID NO:29 from nucleotide 214 to nucleotide 657; the nucleotide sequence of the full-length protein coding sequence of clone vc11_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc11_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(bb) the nucleotide sequence of the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 160 to nucleotide

657, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 160 to nucleotide 657, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 160 to nucleotide 657. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 214 to nucleotide 657, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 214 to nucleotide 657, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 214 to nucleotide 657.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 228 to nucleotide 662;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 327 to nucleotide 662;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc14_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc14_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 228 to nucleotide 662; the nucleotide sequence of SEQ ID NO:31 from nucleotide 327 to nucleotide 662; the nucleotide sequence of the full-length protein coding sequence of clone vc14_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vc14_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bb) the nucleotide sequence of the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 228 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 228 to nucleotide 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 228 to nucleotide 662. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 327 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 327 to nucleotide 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 327 to nucleotide 662.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:32;

(b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 101 to nucleotide 667;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 182 to nucleotide 667;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc16_1 deposited under accession number ATCC 98784;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc16_1 deposited under accession number ATCC 98784;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 101 to nucleotide 667; the nucleotide sequence of SEQ ID NO:33 from nucleotide 182 to nucleotide 667; the nucleotide sequence of the full-length protein coding sequence of clone vc16_1 deposited under accession number ATCC 98784; or the

nucleotide sequence of a mature protein coding sequence of clone vc16_1 deposited under accession number ATCC 98784. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 101 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 101 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 101 to nucleotide 667. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 182 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 182 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 182 to nucleotide 667.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 8 to nucleotide 355;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 134 to nucleotide 355;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc17_1 deposited under accession number ATCC 98784;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc17_1 deposited under accession number ATCC 98784;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 8 to nucleotide 355; the nucleotide sequence of SEQ ID NO:35 from nucleotide 134 to nucleotide 355; the nucleotide sequence of the full-length protein coding sequence of clone vc17_1 deposited under accession number ATCC 98784; or the nucleotide sequence of a mature protein coding sequence of clone vc17_1 deposited under accession number ATCC 98784. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(ab) the nucleotide sequence of the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 8 to nucleotide 355, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 8 to nucleotide 355, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 8 to nucleotide 355. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 134 to nucleotide 355, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 134 to nucleotide 355, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 134 to nucleotide 355.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 1031 to nucleotide 1252;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 1100 to nucleotide 1252;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc21_1 deposited under accession number ATCC 98785;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc21_1 deposited under accession number ATCC 98785;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 1031 to nucleotide 1252; the nucleotide sequence of SEQ ID NO:37 from nucleotide 1100 to nucleotide 1252; the nucleotide sequence of the full-length protein coding sequence of clone vc21_1 deposited under accession number ATCC 98785; or the nucleotide sequence of a mature protein coding sequence of clone vc21_1 deposited under accession number ATCC 98785. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38 from amino acid 29 to amino acid 74. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 1031 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 1031 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide

1031 to nucleotide 1252. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 1100 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 1100 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 1100 to nucleotide 1252.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:38;

(b) the amino acid sequence of SEQ ID NO:38 from amino acid 29 to amino acid 74;

(c) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

(d) the amino acid sequence encoded by the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38 or the amino acid sequence of SEQ ID NO:38 from amino acid 29 to amino acid 74. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 94 to nucleotide 1482;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 214 to nucleotide 1482;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc23_1 deposited under accession number ATCC 98784;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc23_1 deposited under accession number ATCC 98784;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 94 to nucleotide 1482; the nucleotide sequence of SEQ ID NO:39 from nucleotide 214 to nucleotide 1482; the nucleotide sequence of the full-length protein coding sequence of clone vc23_1 deposited under accession number ATCC 98784; or the nucleotide sequence of a mature protein coding sequence of clone vc23_1 deposited under accession number ATCC 98784. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(ab) the nucleotide sequence of the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(bb) the nucleotide sequence of the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 94 to nucleotide 1482, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 94 to nucleotide 1482, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 94 to nucleotide 1482. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 214 to nucleotide 1482, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 214 to nucleotide 1482, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 214 to nucleotide 1482.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 153 to nucleotide 413;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 264 to nucleotide 413;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc25_1 deposited under accession number ATCC 98784;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc25_1 deposited under accession number ATCC 98784;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 153 to nucleotide 413; the nucleotide sequence of SEQ ID NO:41 from nucleotide 264 to nucleotide 413; the nucleotide sequence of the full-length protein coding sequence of clone vc25_1 deposited under accession number ATCC 98784; or the

nucleotide sequence of a mature protein coding sequence of clone vc25_1 deposited under accession number ATCC 98784. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 153 to nucleotide 413, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 153 to nucleotide 413, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 153 to nucleotide 413. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 264 to nucleotide 413, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 264 to nucleotide 413, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 264 to nucleotide 413.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 87 to nucleotide 1409;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 156 to nucleotide 1409;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc26_1 deposited under accession number ATCC 98784;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc26_1 deposited under accession number ATCC 98784;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 87 to nucleotide 1409; the nucleotide sequence of SEQ ID NO:43 from nucleotide 156 to nucleotide 1409; the nucleotide sequence of the full-length protein coding sequence of clone vc26_1 deposited under accession number ATCC 98784; or the nucleotide sequence of a mature protein coding sequence of clone vc26_1 deposited under accession number ATCC 98784. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(bb) the nucleotide sequence of the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 87 to nucleotide 1409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 87 to nucleotide 1409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 87 to nucleotide 1409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 156 to nucleotide 1409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 156 to nucleotide 1409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 156 to nucleotide 1409.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 63 to nucleotide 428;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 156 to nucleotide 428;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 356 to nucleotide 1773;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc30_1 deposited under accession number ATCC 98804;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc30_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 63 to nucleotide 428; the nucleotide sequence of SEQ ID NO:45 from nucleotide 156 to nucleotide 428; the nucleotide sequence of SEQ ID NO:45 from nucleotide 356 to nucleotide 1773; the nucleotide sequence of the full-length protein coding sequence of clone vc30_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vc30_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(ab) the nucleotide sequence of the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 63 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 63 to nucleotide 428, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 63 to nucleotide 428. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 156 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 156 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 156 to nucleotide 428. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 356 to nucleotide 1773, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 356 to nucleotide 1773, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 356 to nucleotide 1773.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:46;

(b) the amino acid sequence of SEQ ID NO:46 from amino acid 1 to amino acid 97;

(c) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and

(d) the amino acid sequence encoded by the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46 or the amino acid sequence of SEQ ID NO:46 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 30 to nucleotide 1799;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 90 to nucleotide 1799;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vd1_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vd1_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 30 to nucleotide 1799; the nucleotide sequence of SEQ ID NO:47 from nucleotide 90 to nucleotide 1799; the nucleotide sequence of the full-length protein coding sequence of clone vd1_1 deposited under accession number ATCC 98748; or the

nucleotide sequence of a mature protein coding sequence of clone vd1_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 290 to amino acid 299 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 30 to nucleotide 1799, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 30 to nucleotide 1799, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 30 to nucleotide 1799. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 90 to nucleotide 1799, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 90 to nucleotide 1799, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 90 to nucleotide 1799.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:48;

(b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 290 to amino acid 299 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 69 to nucleotide 443;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 111 to nucleotide 443;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vd2_1 deposited under accession number ATCC 98748;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vd2_1 deposited under accession number ATCC 98748;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 69 to nucleotide 443; the nucleotide sequence of SEQ ID NO:49 from nucleotide 111 to nucleotide 443; the nucleotide sequence of the full-length protein coding sequence of clone vd2_1 deposited under accession number ATCC 98748; or the nucleotide sequence of a mature protein coding sequence of clone vd2_1 deposited under accession number ATCC 98748. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ab) the nucleotide sequence of the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(bb) the nucleotide sequence of the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 69 to nucleotide 443, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 69 to nucleotide 443, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 69 to nucleotide 443. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 111 to nucleotide 443, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 111 to nucleotide 443, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 111 to nucleotide 443.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:50;

(b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 176 to nucleotide 1249;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 227 to nucleotide 1249;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vd3_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vd3_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 176 to nucleotide 1249; the nucleotide sequence of SEQ ID NO:51 from nucleotide 227 to nucleotide 1249; the nucleotide sequence of the full-length protein coding sequence of clone vd3_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vd3_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(ab) the nucleotide sequence of the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 176 to nucleotide 1249, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 176 to nucleotide 1249, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide

176 to nucleotide 1249. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 227 to nucleotide 1249, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 227 to nucleotide 1249, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 227 to nucleotide 1249.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

(b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 94 to nucleotide 1530;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 145 to nucleotide 1530;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vd4_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vd4_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 94 to nucleotide 1530; the nucleotide sequence of SEQ ID NO:53 from nucleotide 145 to nucleotide 1530; the nucleotide sequence of the full-length protein coding sequence of clone vd4_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vd4_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the

fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 94 to nucleotide 1530, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 94 to nucleotide 1530, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 94 to nucleotide 1530. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 145 to nucleotide 1530, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 145 to nucleotide 1530, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 145 to nucleotide 1530.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1300;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 182 to nucleotide 1300;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ve4_1 deposited under accession number ATCC 98784;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ve4_1 deposited under accession number ATCC 98784;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1300; the nucleotide sequence of SEQ ID NO:55 from nucleotide 182 to nucleotide 1300; the nucleotide sequence of the full-length protein coding sequence of clone ve4_1 deposited under accession number ATCC 98784; or the nucleotide sequence of a mature protein coding sequence of clone ve4_1 deposited under accession number ATCC 98784. In other preferred embodiments, the polynucleotide

encodes the full-length or a mature protein encoded by the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 200 to amino acid 209 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(bb) the nucleotide sequence of the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1300, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1300, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1300. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 182 to nucleotide 1300, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 182 to nucleotide 1300, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 182 to nucleotide 1300.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 200 to amino acid 209 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 57 to nucleotide 785;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 147 to nucleotide 785;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ve8_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ve8_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 57 to nucleotide 785; the nucleotide sequence of SEQ ID NO:57 from nucleotide 147 to nucleotide 785; the nucleotide sequence of the full-length protein coding sequence of clone ve8_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone ve8_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(ab) the nucleotide sequence of the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bb) the nucleotide sequence of the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 57 to nucleotide 785, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 57 to nucleotide 785, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 57 to nucleotide 785. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 147 to nucleotide 785, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 147 to nucleotide 785, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 147 to nucleotide 785.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 64 to nucleotide 1002;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 139 to nucleotide 1002;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vf1_1 deposited under accession number ATCC 98784;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vf1_1 deposited under accession number ATCC 98784;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 64 to nucleotide 1002; the nucleotide sequence of SEQ ID NO:59 from nucleotide 139 to nucleotide 1002; the nucleotide sequence of the full-length protein coding sequence of clone vf1_1 deposited under accession number ATCC 98784; or the nucleotide sequence of a mature protein coding sequence of clone vf1_1 deposited under accession number ATCC 98784. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 151 to amino acid 160 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(ab) the nucleotide sequence of the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(bb) the nucleotide sequence of the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 64 to nucleotide 1002, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 64 to nucleotide 1002, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 64 to nucleotide 1002. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 139 to nucleotide 1002, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from

nucleotide 139 to nucleotide 1002, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 139 to nucleotide 1002.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 151 to amino acid 160 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 588 to nucleotide 995;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 750 to nucleotide 995;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vh1_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vh1_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 588 to nucleotide 995; the nucleotide sequence of SEQ ID NO:61 from nucleotide 750 to nucleotide 995; the nucleotide sequence of the full-length protein coding sequence of clone vh1_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vh1_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 588 to nucleotide

995, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 588 to nucleotide 995, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 588 to nucleotide 995. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 750 to nucleotide 995, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 750 to nucleotide 995, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 750 to nucleotide 995.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 29 to nucleotide 1369;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 104 to nucleotide 1369;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vi1_1 deposited under accession number ATCC 98804;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vi1_1 deposited under accession number ATCC 98804;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 29 to nucleotide 1369; the nucleotide sequence of SEQ ID NO:63 from nucleotide 104 to nucleotide 1369; the nucleotide sequence of the full-length protein coding sequence of clone vi1_1 deposited under accession number ATCC 98804; or the nucleotide sequence of a mature protein coding sequence of clone vi1_1 deposited under accession number ATCC 98804. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 218 to amino acid 227 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 29 to nucleotide 1369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 29 to nucleotide 1369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 29 to nucleotide 1369. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 104 to nucleotide 1369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 104 to nucleotide 1369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 104 to nucleotide 1369.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:64;

(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 218 to amino acid 227 of SEQ ID NO:64.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial,

yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

(a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and

(b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g. , receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "vb2_1"

A polynucleotide of the present invention has been identified as clone "vb2_1". vb2_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb2_1 protein").

The nucleotide sequence of vb2_1 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 15 to 27 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb2_1 protein.

If a frameshift were introduced into the nucleotide sequence of SEQ ID NO:1 by deleting one of the adenine residues at positions 315 and 316, another potential vb2_1 reading frame and predicted amino acid sequence could be encoded by basepairs 126 to 381 of SEQ ID NO:1 and is reported in SEQ ID NO:97. Amino acids 15 to 27 of SEQID NO:97 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28 of SEQ ID NO:97, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb2_1 should be approximately 2342 bp.

The nucleotide sequence disclosed herein for vb2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb2_1 demonstrated at least some similarity with sequences identified as AA308563 (EST179381 HCC cell line (matastasis to liver in mouse) II Homo

sapiens cDNA 5' end, mRNA sequence). Based upon sequence similarity, vb2_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vb3_1"

A polynucleotide of the present invention has been identified as clone "vb3_1". vb3_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb3_1 protein").

The nucleotide sequence of vb3_1 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 16 to 28 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb3_1 should be approximately 2498 bp.

The nucleotide sequence disclosed herein for vb3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb3_1 demonstrated at least some similarity with sequences identified as AA098874 (zn45f11.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550413 3', mRNA sequence) and T26482 (Human gene signature HUMGS08724). Based upon sequence similarity, vb3_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vb4_1"

A polynucleotide of the present invention has been identified as clone "vb4_1". vb4_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb4_1 protein").

The nucleotide sequence of vb4_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 2 to 14 of SEQ ID NO:6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb4_1 should be approximately 2161 bp.

The nucleotide sequence disclosed herein for vb4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb4_1 demonstrated at least some similarity with sequences identified as D88035 (Rat mRNA for glycoprotein specific UDP-glucuronyltransferase, complete cds), N49234 (yy83b10.s1 Homo sapiens cDNA clone 280123 3'), and Q59845 (Human brain Expressed Sequence Tag EST00765). Based upon sequence similarity, vb4_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vb4_1 protein sequence, one centered around amino acid 40 and another around amino acid 80 of SEQ ID NO:6.

Clone "vb5_1"

A polynucleotide of the present invention has been identified as clone "vb5_1". vb5_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb5_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb5_1 protein").

The nucleotide sequence of vb5_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb5_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 7 to 19 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted

leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb5_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb5_1 should be approximately 724 bp.

The nucleotide sequence disclosed herein for vb5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb5_1 demonstrated at least some similarity with sequences identified as AA835218 (ak65a05.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412720 3', mRNA sequence). Based upon sequence similarity, vb5_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vb6_1"

A polynucleotide of the present invention has been identified as clone "vb6_1". vb6_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb6_1 protein").

The nucleotide sequence of vb6_1 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 13 to 25 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb6_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb6_1 should be approximately 2685 bp.

The nucleotide sequence disclosed herein for vb6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb6_1 demonstrated at least some similarity with sequences identified as AA478801 (zv20f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone

754209 3', mRNA sequence). Based upon sequence similarity, vb6_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vb7_1"

A polynucleotide of the present invention has been identified as clone "vb7_1". vb7_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb7_1 protein").

The nucleotide sequence of vb7_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 35 to 47 of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 48. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb7_1 protein.

Another potential vb7_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 1093 to 1577 of SEQ ID NO:11 is reported in SEQ ID NO:98. Amino acids 11 to 23 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24 of SEQ ID NO:98, or are a transmembrane domain. The TopPredII computer program predicts another potential transmembrane domain within the protein sequence of SEQ ID NO:98 centered around amino acid 86 of SEQ ID NO:98. If a frameshift were introduced into the nucleotide sequence of SEQ ID NO:11 approximately between position 1090 and position 1253, the open reading frame of SEQ ID NO:12 could be joined to the open reading frame of SEQ ID NO:98.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb7_1 should be approximately 1730 bp.

The nucleotide sequence disclosed herein for vb7_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb7_1 demonstrated at least some similarity with sequences identified as D13748 (human eukaryotic initiation factor 4AI), M22873 (Mus musculus

protein synthesis initiation factor 4A (eIF-4A) gene, exon 1), and N36589 (yx86f08.r1 Homo sapiens cDNA clone 268647 5'). The predicted amino acid sequence disclosed herein for vb7_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb7_1 protein demonstrated at least some similarity to the sequence identified as AL021839 (hypothetical protein [Schizosaccharomyces pombe]). Based upon sequence similarity, vb7_1 proteins and each similar protein or peptide may share at least some activity.

vb7_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 45 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vb8_1"

A polynucleotide of the present invention has been identified as clone "vb8_1". vb8_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb8_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb8_1 protein").

The nucleotide sequence of vb8_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb8_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb8_1 should be approximately 1363 bp.

The nucleotide sequence disclosed herein for vb8_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb8_1 demonstrated at least some similarity with sequences identified as N57252 (yw93d11.r1 Homo sapiens cDNA clone 259797 5'). The predicted amino acid sequence disclosed herein for vb8_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb8_1 protein demonstrated at least some similarity to sequences identified as AF51239 (probable ubiquitin activating enzyme 2 [Picea mariana]). Based upon sequence similarity, vb8_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain

within the vb8_1 protein sequence centered around amino acid 30 of SEQ ID NO:14. Both the CodonPreference and Testcode computer programs indicate that frameshifts in the nucleotide sequence of SEQ ID NO:13, resulting in the joining of the open reading frame of SEQ ID NO:14 with open reading frames that are more 5' to that of SEQ ID NO:14, are likely.

vb8_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "vb9_1"

A polynucleotide of the present invention has been identified as clone "vb9_1". vb9_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb9_1 protein").

The nucleotide sequence of vb9_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 3 to 15 of SEQ ID NO:16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb9_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb9_1 should be approximately 2996 bp.

The nucleotide sequence disclosed herein for vb9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb9_1 demonstrated at least some similarity with sequences identified as AA446380 (zw58b09.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774233 5', mRNA sequence) and L48440 (Rattus norvegicus collagen type II mRNA, complete cds). The predicted amino acid sequence disclosed herein for vb9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted vb9_1 protein demonstrated at least some similarity to the sequence identified as Z78279 (Collagen alpha1 [Rattus norvegicus]). Based upon sequence similarity, vb9_1 proteins and each similar protein or peptide may share at least some activity.

vb9_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 58 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vc3_1"

A polynucleotide of the present invention has been identified as clone "vc3_1". vc3_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc3_1 protein").

The nucleotide sequence of vc3_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 24 to 36 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc3_1 protein.

Another potential vc3_1 reading frame and predicted amino acid sequence is encoded by basepairs 227 to 703 of SEQ ID NO:17 and is reported in SEQ ID NO:99. Amino acids 83 to 95 of SEQ ID NO:99 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 96, or are a transmembrane domain, and the TopPredII computer program predicts two additional transmembrane domains within the SEQ ID NO:99 amino acid sequence. A frameshift in the nucleotide sequence of SEQ ID NO:17 between about nucleotide 109 to about nucleotide 417 could join together portions of the overlapping reading frames of SEQ ID NO:18 and SEQ ID NO:99.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc3_1 should be approximately 950 bp.

The nucleotide sequence disclosed herein for vc3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc3_1 demonstrated at least some similarity with sequences identified as AA669665 (ac18h12.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone 856871 3'). Based upon sequence similarity, vc3_1 proteins and each similar protein or peptide may share at least some activity.

vc3_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 19 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vc4_1"

A polynucleotide of the present invention has been identified as clone "vc4_1". vc4_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc4_1 protein").

The nucleotide sequence of vc4_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 2 to 14 of SEQ ID NO:20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc4_1 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for vc4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc4_1 demonstrated at least some similarity with sequences identified as Q40970 (Human skeletal muscle ADP-ribosyltransferase gene), U60881 (Mus musculus Yac-2 NAD:arginine ADP-ribosyltransferase mRNA, complete cds), and

W12489 (ma57b11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 314781 5' similar to SW RT61_RAT P17982 ALLOANTIGEN RT6.1 PRECURSOR). The predicted amino acid sequence disclosed herein for vc4_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc4_1 protein demonstrated at least some similarity to sequences identified as R37572 (Rabbit skeletal muscle ADP-ribosyltransferase) and U60881 (Yac-2 NAD arginine ADP-ribosyltransferase [Mus musculus]). ADP-ribosyltransferases are localized to the plasma membrane and are involved in "post-translational modification of proteins in which the ADP-ribose moiety of NAD is transferred to proteins", which is "responsible for the toxicity of some bacterial toxins (e.g. cholera toxin and pertussis toxin)". Based upon sequence similarity, vc4_1 proteins and each similar protein or peptide may share at least some activity.

vc4_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 26 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vc5_1"

A polynucleotide of the present invention has been identified as clone "vc5_1". vc5_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc5_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc5_1 protein").

The nucleotide sequence of vc5_1 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc5_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 63 to 75 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 76. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc5_1 protein.

Another potential vc5_1 reading frame and predicted amino acid sequence is encoded by basepairs 215-376 of SEQ ID NO:21 and is reported in SEQ ID NO:100. Amino

acids 4 to 16 of SEQ ID NO:100 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17 of SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc5_1 should be approximately 1650 bp.

The nucleotide sequence disclosed herein for vc5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc5_1 demonstrated at least some similarity with sequences identified as AA002211 (zh81h07.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 427741 3'). Based upon sequence similarity, vc5_1 proteins and each similar protein or peptide may share at least some activity.

vc5_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 28 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "vc7_1"

A polynucleotide of the present invention has been identified as clone "vc7_1". vc7_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc7_1 protein").

The nucleotide sequence of vc7_1 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 11 to 23 of SEQ ID NO:24 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc7_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for vc7_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "vc9_1"

A polynucleotide of the present invention has been identified as clone "vc9_1". vc9_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc9_1 protein").

The nucleotide sequence of vc9_1 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 10 to 22 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc9_1 protein.

Another potential vc9_1 reading frame and predicted amino acid sequence is encoded by basepairs 1981 to 2619 of SEQ ID NO:25 and is reported in SEQ ID NO:101.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc9_1 should be approximately 4500 bp.

The nucleotide sequence disclosed herein for vc9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc9_1 demonstrated at least some similarity with sequences identified as N66453 (yz41a08.s1 Homo sapiens cDNA clone 285590 3') and Z75407 (Human DNA sequence from cosmid N128A12 on chromosome 22q12-qter contains ESTs, CpG island). Based upon sequence similarity, vc9_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vc9_1 protein sequence at the extreme C-terminus of SEQ ID NO:26.

Clone "vc10_1"

A polynucleotide of the present invention has been identified as clone "vc10_1". vc10_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vc10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc10_1 protein").

The nucleotide sequence of vc10_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 21 to 33 of SEQ ID NO:28 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc10_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for vc10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc10_1 demonstrated at least some similarity with sequences identified as AA398711 (zt75a05.s1 Soares testis NHT Homo sapiens cDNA clone 728144 3') and T24621 (Human gene signature HUMGS06681). Based upon sequence similarity, vc10_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vc10_1 protein sequence centered around amino acid 74 of SEQ ID NO:28. Nuclotides 1103 to 1191 of SEQ ID NO:27 represent a possible intron in the predicted 3' untranslated region of the vc10_1 mRNA molecule.

Clone "vc11_1"

A polynucleotide of the present invention has been identified as clone "vc11_1". vc11_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc11_1 protein").

The nucleotide sequence of vc11_1 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 6 to 18 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the vc11_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc11_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for vc11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc11_1 demonstrated at least some similarity with sequences identified as AA193348 (zr41c08.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 665966 5') and T23590 (Human gene signature HUMGS05443). Based upon sequence similarity, vc11_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vc11_1 protein sequence centered around amino acid 32 of SEQ ID NO:30.

Clone "vc14_1"

A polynucleotide of the present invention has been identified as clone "vc14_1". vc14_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc14_1 protein").

The nucleotide sequence of vc14_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 21 to 33 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc14_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc14_1 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for vc14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc14_1 demonstrated at least some similarity with sequences identified as AA258182 (zs35f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE

687209 3'). The predicted amino acid sequence disclosed herein for vc14_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc14_1 protein demonstrated at least some similarity to sequences identified as AC002339 (BAC T11A7 [Arabidopsis thaliana]) and Z71266 (R06C7.6 [Caenorhabditis elegans]). Based upon sequence similarity, vc14_1 proteins and each similar protein or peptide may share at least some activity.

vc14_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vc16_1"

A polynucleotide of the present invention has been identified as clone "vc16_1". vc16_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc16_1 protein").

The nucleotide sequence of vc16_1 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 15 to 27 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc16_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc16_1 should be approximately 1256 bp.

The nucleotide sequence disclosed herein for vc16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc16_1 demonstrated at least some similarity with sequences identified as AA776882 (ac40a09.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 858904 3' similar to SW XB3_XENLA Q09004 STATHMIN-LIKE PROTEIN XB3, mRNA sequence), AF026528 (Rattus norvegicus stathmin-like-protein

RB3 mRNA, complete cds), and AF026529 (Rattus norvegicus stathmin-like-protein splice variant RB3' mRNA, complete cds). The predicted amino acid sequence disclosed herein for vc16_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc16_1 protein demonstrated at least some similarity to sequences identified as AF026528 (stathmin-like-protein RB3 [Rattus norvegicus]). While stathmin itself is intracellular, stathmin-related protein RB3 (as well as related proteins SCG10 in rat and XB3 in *Xenopus*) is membrane-associated and has been isolated in the membrane fraction from cell cultures. RB3 is expressed in neural tissue and may be involved in the expression of differentiated neuronal function. Based upon sequence similarity, vc16_1 proteins and each similar protein or peptide may share at least some activity.

vc16_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 89 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "vc17_1"

A polynucleotide of the present invention has been identified as clone "vc17_1". vc17_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc17_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc17_1 protein").

The nucleotide sequence of vc17_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc17_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. Amino acids 30 to 42 of SEQ ID NO:36 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc17_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc17_1 should be approximately 1783 bp.

The nucleotide sequence disclosed herein for vc17_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc17_1 demonstrated at least some similarity with sequences identified as N73805 (yz80g02.s1 Homo sapiens cDNA clone 289394 3'), and T24437 (Human gene signature HUMGS06471). Based upon sequence similarity, vc17_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vc17_1 protein sequence centered around amino acid 60 of SEQ ID NO:36.

Clone "vc21_1"

A polynucleotide of the present invention has been identified as clone "vc21_1". vc21_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc21_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc21_1 protein").

The nucleotide sequence of vc21_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 11 to 23 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc21_1 protein.

Another potential vc21_1 reading frame and predicted amino acid sequence is encoded by basepairs 796 to 1014 of SEQ ID NO:37 and is reported in SEQ ID NO:102.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc21_1 should be approximately 1773 bp.

The nucleotide sequence disclosed herein for vc21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc21_1 demonstrated at least some similarity with sequences identified as W85910 (zh52b10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 415675 3', mRNA sequence) and T24609 (Human gene signature

HUMGS06668). Based upon sequence similarity, vc21_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vc23_1"

A polynucleotide of the present invention has been identified as clone "vc23_1". vc23_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc23_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc23_1 protein").

The nucleotide sequence of vc23_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 28 to 40 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc23_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc23_1 should be approximately 1998 bp.

The nucleotide sequence disclosed herein for vc23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc23_1 demonstrated at least some similarity with sequences identified as AA580484 (nn22a05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1084592 similar to TR:G1209718 G1209718 HYPOTHETICAL 50.1 KD PROTEIN, mRNA sequence), T25530 (Human gene signature HUMGS07700), U41293 (Saccharomyces cerevisiae putative serine/threonine protein kinase gene, putative ribosomal protein L25 gene, and malate dehydrogenase (MDH2) gene, complete cds), and Z74866 (S.cerevisiae chromosome XV reading frame ORF YOL124c). The predicted amino acid sequence disclosed herein for vc23_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc23_1 protein demonstrated at least some similarity to sequences identified as U41293 (unknown [Saccharomyces cerevisiae]) and Z74866 (ORF YOL124c [Saccharo-

myces cerevisiae]). Based upon sequence similarity, vc23_1 proteins and each similar protein or peptide may share at least some activity. The vc23_1 protein contains a "N-6 adenine-specific DNA methylases signature" motif. The TopPredII computer program predicts a potential transmembrane domain within the vc23_1 protein sequence centered around amino acid 232 of SEQ ID NO:40.

vc23_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 51 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vc25_1"

A polynucleotide of the present invention has been identified as clone "vc25_1". vc25_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc25_1 protein").

The nucleotide sequence of vc25_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 25 to 37 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc25_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc25_1 should be approximately 1653 bp.

The nucleotide sequence disclosed herein for vc25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc25_1 demonstrated at least some similarity with sequences identified as N21690 (yx63h08.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone 266463 3', mRNA sequence) and T25257 (Human gene signature HUMGS07418). Based upon sequence similarity, vc25_1 proteins and each similar protein or peptide may share at least some activity.

vc25_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 15 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vc26_1"

A polynucleotide of the present invention has been identified as clone "vc26_1". vc26_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc26_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc26_1 protein").

The nucleotide sequence of vc26_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc26_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44. Amino acids 11 to 23 of SEQ ID NO:44 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc26_1 protein.

If the "G" residue at position 669 of SEQ ID NO:43 were deleted to create a frameshft, another potential vc26_1 reading frame and predicted amino acid sequence could be encoded by what would then be basepairs 87 to 992 of the deletion-containing version of SEQ ID NO:43. This potential vc26_1 reading frame and predicted amino acid sequence is reported in SEQ ID NO:103. Amino acids 11 to 23 of both SEQ ID NO:44 and SEQ ID NO:103 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc26_1 should be approximately 1982 bp.

The nucleotide sequence disclosed herein for vc26_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc26_1 demonstrated at least some similarity with sequences identified as AA877534 (nr01g08.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1160606 3', mRNA sequence) and T25645 (Human gene signature HUMGS07835). The predicted vc26_1 protein of SEQ ID NO:10 contains an immuno-

globulins and major histocompatibility complex proteins signature at amino acid 131. Based upon sequence similarity, vc26_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts seven additional potential transmembrane domains within the vc26_1 protein sequence, centered around amino acids 60, 100, 120, 160, 210, 250, and 290 of SEQ ID NO:44, respectively.

Clone "vc30_1"

A polynucleotide of the present invention has been identified as clone "vc30_1". vc30_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc30_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc30_1 protein").

The nucleotide sequence of vc30_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc30_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 19 to 31 of SEQ ID NO:46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc30_1 protein.

If a frameshift were introduced in the nucleotide sequence of SEQ ID NO:45 by deleting the cytosine residue at position 1393, another potential vc30_1 reading frame and predicted amino acid sequence could be encoded by what would then be basepairs 1317 to 1659 of SEQ ID NO:45 and is reported in SEQ ID NO:104.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc30_1 should be approximately 1887 bp.

The nucleotide sequence disclosed herein for vc30_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc30_1 demonstrated at least some similarity with sequences identified as AA496421 (zv37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755814 5', mRNA sequence). The predicted amino acid sequence disclosed herein for vc30_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc30_1 protein demonstrated at least

some similarity to sequences identified as AF047760 (phosphatidic acid phosphohydrolase type 2c [Homo sapiens]). Based upon sequence similarity, vc30_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vc30_1 protein sequence centered around amino acid 55 of SEQ ID NO:46.

Clone "vd1_1"

A polynucleotide of the present invention has been identified as clone "vd1_1". vd1_1 was isolated from a human adult skin cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vd1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vd1_1 protein").

The nucleotide sequence of vd1_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vd1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 8 to 20 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vd1_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vd1_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for vd1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vd1_1 demonstrated at least some similarity with sequences identified as AA582963 (nn72e02.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE 1089434) and AC002389 (Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence). Based upon sequence similarity, vd1_1 proteins and each similar protein or peptide may share at least some activity. There is an 18-residue amino acid stretch (with an approximate consensus sequence shown in SEQ ID NO:105 (HHAAGQAGNEAGRFGQGV)) that is almost tandemly repeated 15 times in the vd1_1 protein. Nucleotides 406-1668 of SEQ ID NO:47, which encode a region of SEQ ID

NO:48 that includes the 18-residue amino acid repeats, may represent an alternatively spliced region in mRNA molecules transcribed from the vd1_1 gene.

vd1_protein was expressed in a COS cell expression system, and an expressed protein band of approximately 55 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "vd2_1"

A polynucleotide of the present invention has been identified as clone "vd2_1". vd2_1 was isolated from a human adult skin cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vd2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vd2_1 protein").

The nucleotide sequence of vd2_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vd2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 2 to 14 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vd2_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vd2_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for vd2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vd2_1 demonstrated at least some similarity with sequences identified as H03945 (yj44c02.s1 Homo sapiens cDNA clone 151586 3'). Based upon sequence similarity, vd2_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vd2_1 protein sequence centered around amino acid 115 of SEQ ID NO:50.

Clone "vd3_1"

A polynucleotide of the present invention has been identified as clone "vd3_1". vd3_1 was isolated from a human adult skin cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vd3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vd3_1 protein").

The nucleotide sequence of vd3_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vd3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 5 to 17 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vd3_1 protein.

If a frameshift were introduced into the nucleotide sequence of SEQ ID NO:19 by inserting an adenine or thymine residue at position 1132 or 1133, another potential vd3_1 reading frame and predicted amino acid sequence could be encoded by basepairs 176 to 1281 of SEQ ID NO:51 and is reported in SEQ ID NO:106. Amino acids 5 to 17 of SEQID NO:106 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18 of SEQ ID NO:106, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vd3_1 should be approximately 1537 bp.

The nucleotide sequence disclosed herein for vd3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vd3_1 demonstrated at least some similarity with sequences identified as AA873028 (ob11e05.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE 1323392 3', mRNA sequence), AC002389 (Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence), and AD001502 (Homo sapiens DNA from chromosome 19-cosmid f21246, genomic sequence). Based upon sequence similarity, vd3_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional possible transmembrane domain within the vd3_1 protein sequence centered around amino acid

290 of SEQ ID NO:52. The vd3_1 protein is apparently a splice variant of the vd4_1 protein described below.

vd3_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 42 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vd4_1"

A polynucleotide of the present invention has been identified as clone "vd4_1". vd4_1 was isolated from a human adult skin cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vd4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vd4_1 protein").

The nucleotide sequence of vd4_1 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vd4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 5 to 17 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vd4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vd4_1 should be approximately 1897 bp.

The nucleotide sequence disclosed herein for vd4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vd4_1 demonstrated at least some similarity with sequences identified as AA706316 (ah28e11.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1240172 3', mRNA sequence), AC002389 (Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence), and AD001502 (Homo sapiens DNA from chromosome 19-cosmid f21246, genomic sequence). Based upon sequence similarity, vd4_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional possible transmembrane domain within the vd4_1 protein sequence centered around amino acid

290 of SEQ ID NO:54. The vd4_1 protein is apparently a splice variant of the vd3_1 protein described above.

vd4_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 54 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "ve4_1"

A polynucleotide of the present invention has been identified as clone "ve4_1". ve4_1 was isolated from a human adult brain (Alzheimer's hippocampus level 7) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ve4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ve4_1 protein").

The nucleotide sequence of ve4_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ve4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 25 to 37 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ve4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ve4_1 should be approximately 1578 bp.

The nucleotide sequence disclosed herein for ve4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ve4_1 demonstrated at least some similarity with sequences identified as AA707153 (zj33f10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 452107 3' similar to TR P70295 P70295 AUP1 PRECURSOR, mRNA sequence) and U41736 (Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds). The predicted amino acid sequence disclosed herein for ve4_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ve4_1 protein demonstrated at least

some similarity to the sequence identified as U41736 (ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]). Based upon sequence similarity, ve4_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the ve4_1 protein sequence, one centered around amino acid 110 and another around amino acid 210 of SEQ ID NO:56.

ve4_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 41 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ve8_1"

A polynucleotide of the present invention has been identified as clone "ve8_1". ve8_1 was isolated from a human adult brain (Alzheimer's hippocampus level 7) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ve8_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ve8_1 protein").

The nucleotide sequence of ve8_1 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ve8_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 18 to 30 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ve8_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ve8_1 should be approximately 2093 bp.

The nucleotide sequence disclosed herein for ve8_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ve8_1 demonstrated at least some similarity with sequences identified as AC004126 (Homo sapiens Chromosome 11q12 pac pDJ606g6; HTGS phase 1, 17 unordered pieces). Based upon sequence similarity, ve8_1 proteins and each similar

protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the ve8_1 protein sequence, centered around amino acids 94, 147, 150, and 193 of SEQ ID NO:58, respectively.

Clone "vf1_1"

A polynucleotide of the present invention has been identified as clone "vf1_1". vf1_1 was isolated from a human adult heart cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vf1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vf1_1 protein").

The nucleotide sequence of vf1_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vf1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 13 to 25 of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vf1_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vf1_1 should be approximately 1382 bp.

The nucleotide sequence disclosed herein for vf1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vf1_1 demonstrated at least some similarity with sequences identified as AA349531 (EST56314 Infant brain Homo sapiens cDNA 5' end, mRNA sequence) and AA532642 (nj17c07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE 986604, mRNA sequence). Based upon sequence similarity, vf1_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vf1_1 protein sequence centered around amino acid 138 of SEQ ID NO:60.

vf1_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 40 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vh1_1"

A polynucleotide of the present invention has been identified as clone "vh1_1". vh1_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vh1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vh1_1 protein").

The nucleotide sequence of vh1_1 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vh1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino acids 42 to 54 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 55. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vh1_1 protein.

Another potential vh1_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 833 to 1054 of SEQ ID NO:61 is reported in SEQ ID NO:107. Amino acids 22 to 34 of SEQ ID NO:107 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35 of SEQ ID NO:107, or are a transmembrane domain. If a frameshift were introduced into the nucleotide sequence of SEQ ID NO:61 approximately between position 830 and position 998, the open reading frame of SEQ ID NO:62 could be joined to the open reading frame of SEQ ID NO:107.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vh1_1 should be approximately 1529 bp.

The nucleotide sequence disclosed herein for vh1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vh1_1 demonstrated at least some similarity with sequences identified as AA927736 (om72h10.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone

IMAGE:1552771 3', mRNA sequence). Based upon sequence similarity, vh1_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vi1_1"

A polynucleotide of the present invention has been identified as clone "vi1_1". vi1_1 was isolated from a human adult aorta cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vi1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vi1_1 protein").

The nucleotide sequence of vi1_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vi1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 13 to 25 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vi1_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vi1_1 should be approximately 2348 bp.

The nucleotide sequence disclosed herein for vi1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vi1_1 demonstrated at least some similarity with sequences identified as AA411541 (zv30a03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755116 5' similar to WP:F07H5.11 CE03160) and T21484 (Human gene signature HUMGS02856). The predicted amino acid sequence disclosed herein for vi1_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vi1_1 protein demonstrated at least some similarity to the sequence identified as Z68314 (F46C5.9 [Caenorhabditis elegans]). The amino acid sequence of the predicted vi1_1 protein indicates that it may contain a beta-transducin family Trp-Asp repeat signature (WD-40) motif centered around residue 300 of SEQ ID NO:28. The WD-40 motif is thought to be a widely distributed protein-protein interaction domain. Based upon sequence similarity, vi1_1 proteins and each similar

protein or peptide may share at least some activity. The TopPredII computer program predicts two additional possible transmembrane domains within the vil_1 protein sequence, one centered around amino acid 200 and another around amino acid 340 of SEQ ID NO:64.

vil_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 45 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Deposit of Clones

Clones vc3_1, vc4_1, vc5_1, vc7_1, vc9_1, vc10_1, vc11_1, vc14_1, vd1_1, and vd2_1 were deposited on April 24, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98748, from which each clone comprising a particular polynucleotide is obtainable.

Clone vc21_1 was deposited on June 10, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number ATCC 98785, from which each clone comprising a particular polynucleotide is obtainable.

Clones vc16_1, vc17_1, vc23_1, vc25_1, vc26_1, ve4_1, and vf1_1 were deposited on June 10, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98784, from which each clone comprising a particular polynucleotide is obtainable.

Clones vb2_1, vb3_1, vb4_1, vb5_1, vb6_1, vb7_1, vb8_1, vb9_1, vc30_1, vd3_1, vd4_1, ve8_1, vh1_1, and vi1_1 were deposited on July 1, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98804, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in these composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

Clone	Probe Sequence
vb2_1	SEQ ID NO:65
vb3_1	SEQ ID NO:66
vb4_1	SEQ ID NO:67
vb5_1	SEQ ID NO:68
vb6_1	SEQ ID NO:69
vb7_1	SEQ ID NO:70
vb8_1	SEQ ID NO:71
vb9_1	SEQ ID NO:72
vc3_1	SEQ ID NO:73
vc4_1	SEQ ID NO:74

vc5_1	SEQ ID NO:75
vc7_1	SEQ ID NO:76
vc9_1	SEQ ID NO:77
vc10_1	SEQ ID NO:78
vc11_1	SEQ ID NO:79
vc14_1	SEQ ID NO:80
vc16_1	SEQ ID NO:81
vc17_1	SEQ ID NO:82
vc21_1	SEQ ID NO:83
vc23_1	SEQ ID NO:84
vc25_1	SEQ ID NO:85
vc26_1	SEQ ID NO:86
vc30_1	SEQ ID NO:87
vd1_1	SEQ ID NO:88
vd2_1	SEQ ID NO:89
vd3_1	SEQ ID NO:90
vd4_1	SEQ ID NO:91
ve4_1	SEQ ID NO:92
ve8_1	SEQ ID NO:93
vf1_1	SEQ ID NO:94
vh1_1	SEQ ID NO:95
vi1_1	SEQ ID NO:96

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoaramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramadite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

(a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

(b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ-^{32}P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 µl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 µg/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately

labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address http://www.ncbi.nlm.nih.gov/UniGene/, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988,

Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmsmbrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of*

Molecular Biology **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* **3**: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from ftp://blast.wustl.edu/blast/executables. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence

identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes, Gorilla gorilla, Pongo pygmaeus, Hylobates concolor, Macaca mulatta, Papio papio, Papio hamadryas, Cercopithecus aethiops, Cebus capucinus, Aotus trivirgatus, Sanguinus oedipus, Microcebus murinus, Mus musculus, Rattus norvegicus, Cricetulus griseus, Felis catus, Mustela vison, Canis familiaris, Oryctolagus cuniculus, Bos taurus, Ovis aries, Sus scrofa,* and *Equus caballus,* for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly

stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp)‡	Hybridization Temperature and Buffer†	Wash Temperature and Buffer†
A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
B	DNA:DNA	<50	T_B*; 1xSSC	T_B*; 1xSSC
C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
D	DNA:RNA	<50	T_D*; 1xSSC	T_D*; 1xSSC
E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
F	RNA:RNA	<50	T_F*; 1xSSC	T_F*; 1xSSC
G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
H	DNA:DNA	<50	T_H*; 4xSSC	T_H*; 4xSSC
I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
J	DNA:RNA	<50	T_J*; 4xSSC	T_J*; 4xSSC
K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
L	RNA:RNA	<50	T_L*; 2xSSC	T_L*; 2xSSC
M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
N	DNA:DNA	<50	T_N*; 6xSSC	T_N*; 6xSSC
O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
P	DNA:RNA	<50	T_P*; 6xSSC	T_P*; 6xSSC
Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
R	RNA:RNA	<50	T_R*; 4xSSC	T_R*; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6($\log_{10}$[Na^+]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell

strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces* strains, *Candida,* or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium,* or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin

(TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art

(see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those

described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991;

Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic

lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this

matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, *89*:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II

molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines,

thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359,

1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc.., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and

other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac)

and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for

advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and

beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the

cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism,

anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to

a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted

antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, Monoclonal antibodies: principles and practice, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in Current Protocols in Immunology, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, supra; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in Current Protocols in Immunology, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* **14**: 845-851; Mendez *et al.*, 1997, *Nature Genetics* **15**: 146-156 (erratum *Nature Genetics* **16**: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions

associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-

aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in

the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:1;

(b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 126 to nucleotide 485;

(c) the nucleotide sequence of SEQ ID NO:1 from nucleotide 207 to nucleotide 485;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb2_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb2_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:1.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.

4. The host cell of claim 3, wherein said cell is a mammalian cell.

5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

(a) growing a culture of a host cell transformed with the polynucleotide of claim 2 in a suitable culture medium; and

(b) purifying said protein from the culture.

6. A protein produced according to the process of claim 5.

7. An isolated polynucleotide encoding the protein of claim 6.

8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804.

9. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb2_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:3;

(b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 130 to nucleotide 2286;

(c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 214 to nucleotide 2286;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb3_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb3_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb3_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:5;

(b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 172 to nucleotide 522;

(c) the nucleotide sequence of SEQ ID NO:5 from nucleotide 214 to nucleotide 522;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb4_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb4_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb4_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:7;

(b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 119 to nucleotide 502;

(c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 176 to nucleotide 502;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb5_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb5_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb5_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:9;

(b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 128 to nucleotide 436;

(c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 203 to nucleotide 436;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb6_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb6_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb6_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:11;

(b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 138 to nucleotide 1250;

(c) the nucleotide sequence of SEQ ID NO:11 from nucleotide 279 to nucleotide 1250;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb7_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb7_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb7_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:13;

(b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 615 to nucleotide 869;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vb8_1 deposited under accession number ATCC 98804;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb8_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:15;

(b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 1470;

(c) the nucleotide sequence of SEQ ID NO:15 from nucleotide 193 to nucleotide 1470;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb9_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb9_1 deposited under accession number ATCC 93804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb9_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:17;

(b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 109 to nucleotide 414;

(c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 217 to nucleotide 414;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc3_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc3_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc3_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:19;

(b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 169 to nucleotide 840;

(c) the nucleotide sequence of SEQ ID NO:19 from nucleotide 211 to nucleotide 840;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc4_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc4_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc4_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:21;

(b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 508 to nucleotide 951;

(c) the nucleotide sequence of SEQ ID NO:21 from nucleotide 733 to nucleotide 951;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc5_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc5_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc5_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:23;

(b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 125 to nucleotide 493;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vc7_1 deposited under accession number ATCC 98748;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc7_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:25;

(b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 33 to nucleotide 407;

(c) the nucleotide sequence of SEQ ID NO:25 from nucleotide 99 to nucleotide 407;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc9_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc9_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc9_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:27;

(b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 176 to nucleotide 871;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vc10_1 deposited under accession number ATCC 98748;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc10_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:29;

(b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 160 to nucleotide 657;

(c) the nucleotide sequence of SEQ ID NO:29 from nucleotide 214 to nucleotide 657;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc11_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc11_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc11_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:31;

(b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 228 to nucleotide 662;

(c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 327 to nucleotide 662;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc14_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc14_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:32;

(b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc14_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:33;

(b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 101 to nucleotide 667;

(c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 182 to nucleotide 667;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc16_1 deposited under accession number ATCC 98784;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc16_1 deposited under accession number ATCC 98784;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc16_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:35;

(b) the nucleotide sequence of SEQ ID NO:35 from nucleotide 8 to nucleotide 355;

(c) the nucleotide sequence of SEQ ID NO:35 from nucleotide 134 to nucleotide 355;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc17_1 deposited under accession number ATCC 98784;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc17_1 deposited under accession number ATCC 98784;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc17_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:37;

(b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 1031 to nucleotide 1252;

(c) the nucleotide sequence of SEQ ID NO:37 from nucleotide 1100 to nucleotide 1252;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc21_1 deposited under accession number ATCC 98785;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc21_1 deposited under accession number ATCC 98785;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:38;

(b) the amino acid sequence of SEQ ID NO:38 from amino acid 29 to amino acid 74;

(c) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

(d) the amino acid sequence encoded by the cDNA insert of clone vc21_1 deposited under accession number ATCC 98785;

the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:39;

(b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 94 to nucleotide 1482;

(c) the nucleotide sequence of SEQ ID NO:39 from nucleotide 214 to nucleotide 1482;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc23_1 deposited under accession number ATCC 98784;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc23_1 deposited under accession number ATCC 98784;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc23_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:41;

(b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 153 to nucleotide 413;

(c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 264 to nucleotide 413;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc25_1 deposited under accession number ATCC 98784;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc25_1 deposited under accession number ATCC 98784;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc25_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:43;

(b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 87 to nucleotide 1409;

(c) the nucleotide sequence of SEQ ID NO:43 from nucleotide 156 to nucleotide 1409;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc26_1 deposited under accession number ATCC 98784;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc26_1 deposited under accession number ATCC 98784;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc26_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:45;

(b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 63 to nucleotide 428;

(c) the nucleotide sequence of SEQ ID NO:45 from nucleotide 156 to nucleotide 428;

(d) the nucleotide sequence of SEQ ID NO:45 from nucleotide 356 to nucleotide 1773;

(e) the nucleotide sequence of the full-length protein coding sequence of clone vc30_1 deposited under accession number ATCC 98804;

(f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

(g) the nucleotide sequence of a mature protein coding sequence of clone vc30_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

(i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and

(l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:46;

(b) the amino acid sequence of SEQ ID NO:46 from amino acid 1 to amino acid 97;

(c) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and

(d) the amino acid sequence encoded by the cDNA insert of clone vc30_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:47;

(b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 30 to nucleotide 1799;

(c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 90 to nucleotide 1799;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vd1_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vd1_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:48;

(b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd1_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:49;

(b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 69 to nucleotide 443;

(c) the nucleotide sequence of SEQ ID NO:49 from nucleotide 111 to nucleotide 443;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vd2_1 deposited under accession number ATCC 98748;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

(f) the nucleotide sequence of a mature protein coding sequence of clone vd2_1 deposited under accession number ATCC 98748;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:50;

(b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd2_1 deposited under accession number ATCC 98748;

the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:51;

(b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 176 to nucleotide 1249;

(c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 227 to nucleotide 1249;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vd3_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vd3_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

(b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd3_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:53;

(b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 94 to nucleotide 1530;

(c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 145 to nucleotide 1530;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vd4_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vd4_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone vd4_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:55;

(b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1300;

(c) the nucleotide sequence of SEQ ID NO:55 from nucleotide 182 to nucleotide 1300;

(d) the nucleotide sequence of the full-length protein coding sequence of clone ve4_1 deposited under accession number ATCC 98784;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

(f) the nucleotide sequence of a mature protein coding sequence of clone ve4_1 deposited under accession number ATCC 98784;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone ve4_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:57;

(b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 57 to nucleotide 785;

(c) the nucleotide sequence of SEQ ID NO:57 from nucleotide 147 to nucleotide 785;

(d) the nucleotide sequence of the full-length protein coding sequence of clone ve8_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone ve8_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone ve8_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:59;

(b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 64 to nucleotide 1002;

(c) the nucleotide sequence of SEQ ID NO:59 from nucleotide 139 to nucleotide 1002;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vf1_1 deposited under accession number ATCC 98784;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

(f) the nucleotide sequence of a mature protein coding sequence of clone vf1_1 deposited under accession number ATCC 98784;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone vf1_1 deposited under accession number ATCC 98784;

the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:61;

(b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 588 to nucleotide 995;

(c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 750 to nucleotide 995;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vh1_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vh1_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone vh1_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:63;

(b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 29 to nucleotide 1369;

(c) the nucleotide sequence of SEQ ID NO:63 from nucleotide 104 to nucleotide 1369;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vi1_1 deposited under accession number ATCC 98804;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

(f) the nucleotide sequence of a mature protein coding sequence of clone vi1_1 deposited under accession number ATCC 98804;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:

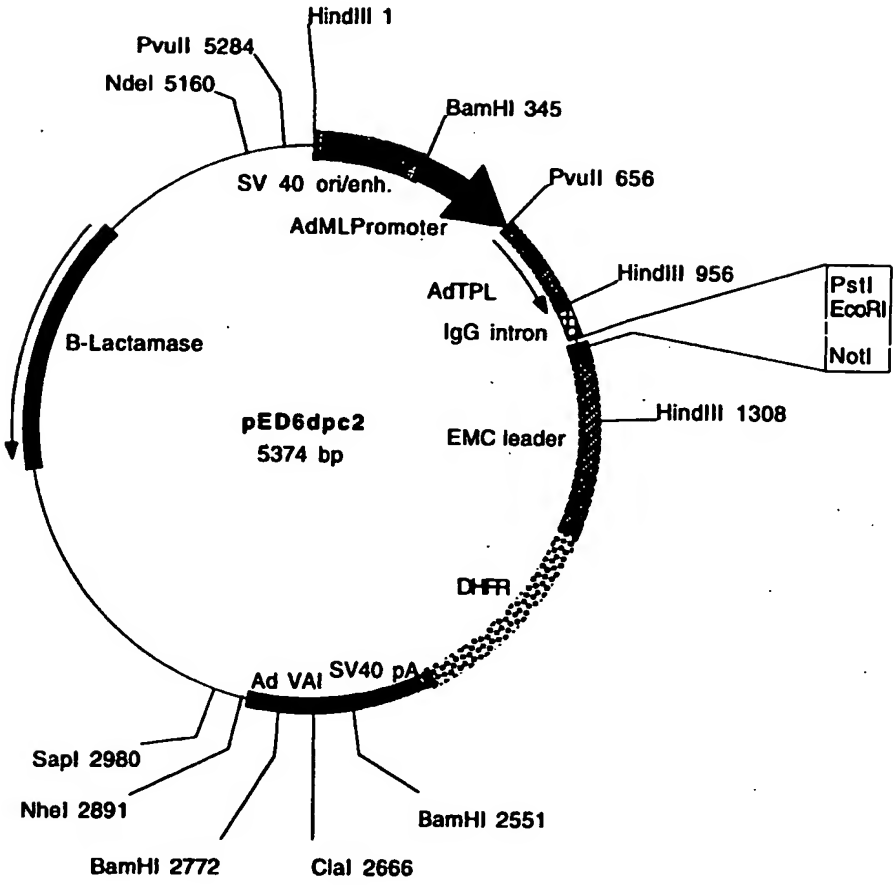
(a) the amino acid sequence of SEQ ID NO:64;

(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone vi1_1 deposited under accession number ATCC 98804;

the protein being substantially free from other mammalian proteins.

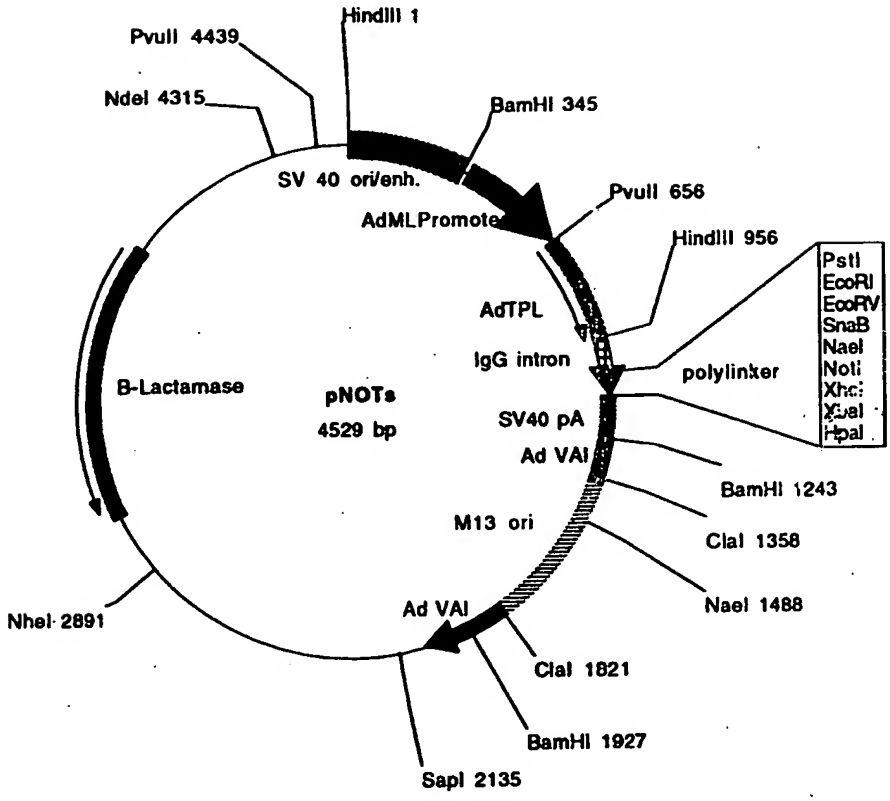
FIGURE 1A



Plasmid name: pED6dpc2
Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



Plasmid name: pNOTs
Plasmid size: 4529 bp

Comments/References: pNOTs is a derivative of pMT2 (Kaufman et al,1989. Mol.Cell.Biol.9:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the ClaI site. SST cDNAs are cloned between EcoRI and NotI

SEQUENCE LISTING

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Hoffman, Heidi
Hall, Jeff
Rapiejko, Peter
AlphaGene, Inc.

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<212> PRT
<213> Homo sapiens

<400> 4

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Phe Ser Gly Leu Ile Leu Leu Ser Glu Leu Leu Pro Leu Pro Leu Pro
             20                  25                  30

Met Gln Thr Thr Gln Val Ile Glu Pro His Asp Ile Ser Val Ala Leu
         35                  40                  45

Asn Thr Arg Lys Leu Trp Ser Met His Leu His Val Gln Ala Lys Leu
     50                  55                  60

Leu Gln Glu Ile Val Arg Ser Phe Ser Gly Thr Thr Cys Gln Pro Ile
 65                  70                  75                  80

Gln His Met Leu Arg Arg Ile Cys Val Gln Leu Cys Asp Leu Ala Ser
                 85                  90                  95

Pro Thr Ala Leu Leu Ile Met Arg Thr Val Leu Asp Leu Ile Val Glu
            100                 105                 110

Asp Leu Gln Ser Thr Ser Glu Asp Lys Glu Lys Gln Tyr Thr Ser Gln
        115                 120                 125

Thr Thr Arg Leu Leu Ala Leu Leu Asp Ala Leu Ala Ser His Lys Ala
    130                 135                 140

Cys Lys Leu Ala Ile Leu His Leu Ile Asn Gly Thr Ile Lys Gly Asp
145                 150                 155                 160
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Glu Arg Tyr Ala Glu Ile Phe Gln Asp Leu Leu Ala Leu Val Arg Ser
                165                 170                 175

Pro Gly Asp Ser Val Ile Arg Gln Gln Cys Val Glu Tyr Val Thr Ser
            180                 185                 190

Ile Leu Gln Ser Leu Cys Asp Gln Asp Ile Ala Leu Ile Leu Pro Ser
        195                 200                 205

Ser Ser Glu Gly Ser Ile Ser Glu Leu Glu Gln Leu Ser Asn Ser Leu
    210                 215                 220

Pro Asn Lys Glu Leu Met Thr Ser Ile Cys Asp Cys Leu Leu Ala Thr
225                 230                 235                 240

Leu Ala Asn Ser Glu Ser Ser Tyr Asn Cys Leu Leu Thr Cys Val Arg
                245                 250                 255

Thr Met Met Phe Leu Ala Glu His Asp Tyr Gly Leu Phe His Leu Lys
            260                 265                 270

Ser Ser Leu Arg Lys Asn Ser Ser Ala Leu His Ser Leu Leu Lys Arg
        275                 280                 285

Val Val Ser Thr Phe Ser Lys Asp Thr Gly Glu Leu Ala Ser Ser Phe
    290                 295                 300

Leu Glu Phe Met Arg Gln Ile Leu Asn Ser Asp Thr Ile Gly Cys Cys
305                 310                 315                 320

Gly Asp Asp Asn Gly Leu Met Glu Val Glu Gly Ala His Thr Ser Arg
                325                 330                 335

Thr Met Ser Ile Asn Ala Ala Glu Leu Lys Gln Leu Leu Gln Ser Lys
            340                 345                 350

Glu Glu Ser Pro Glu Asn Leu Phe Leu Glu Leu Glu Lys Leu Val Leu
        355                 360                 365

Glu His Ser Lys Asp Asp Asp Asn Leu Asp Ser Leu Leu Asp Ser Val
    370                 375                 380

Val Gly Leu Lys Gln Met Leu Glu Ser Ser Gly Asp Pro Leu Pro Leu
385                 390                 395                 400

Ser Asp Gln Asp Val Glu Pro Val Leu Ser Ala Pro Glu Ser Leu Gln
                405                 410                 415

Asn Leu Phe Asn Asn Arg Thr Ala Tyr Val Leu Ala Asp Val Met Asp
            420                 425                 430

Asp Gln Leu Lys Ser Met Trp Phe Thr Pro Phe Gln Ala Glu Glu Ile
        435                 440                 445

Asp Thr Asp Leu Asp Leu Val Lys Val Asp Leu Ile Glu Leu Ser Glu
    450                 455                 460

Lys Cys Cys Ser Asp Phe Asp Leu His Ser Glu Leu Glu Arg Ser Phe
465                 470                 475                 480
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```
Leu Ser Glu Pro Ser Ser Pro Gly Arg Thr Lys Thr Thr Lys Gly Phe
                485                 490                 495

Lys Leu Gly Lys His Lys His Glu Thr Phe Ile Thr Ser Ser Gly Lys
            500                 505                 510

Ser Glu Tyr Ile Glu Pro Ala Lys Arg Ala His Val Val Pro Pro Pro
        515                 520                 525

Arg Gly Arg Gly Arg Gly Gly Phe Gly Gln Gly Ile Arg Pro His Asp
    530                 535                 540

Ile Phe Arg Gln Arg Lys Gln Asn Thr Ser Arg Pro Pro Ser Met His
545                 550                 555                 560

Val Asp Asp Phe Val Ala Ala Glu Ser Lys Glu Val Val Pro Gln Asp
                565                 570                 575

Gly Ile Pro Pro Pro Lys Arg Pro Leu Lys Ala Ser Gln Lys Ile Ser
            580                 585                 590

Ser Arg Gly Gly Phe Ser Gly Asn Arg Gly Gly Arg Gly Ala Phe His
        595                 600                 605

Ser Gln Asn Arg Phe Phe Thr Pro Pro Ala Ser Lys Gly Asn Tyr Ser
    610                 615                 620

Arg Arg Glu Gly Thr Arg Gly Ser Ser Trp Ser Ala Gln Asn Thr Pro
625                 630                 635                 640

Arg Gly Asn Tyr Asn Glu Ser Arg Gly Gly Gln Ser Asn Phe Asn Arg
                645                 650                 655

Gly Pro Leu Pro Pro Leu Arg Pro Leu Ser Ser Thr Gly Tyr Arg Pro
            660                 665                 670

Ser Pro Arg Asp Arg Ala Ser Arg Gly Arg Gly Gly Leu Gly Pro Ser
        675                 680                 685

Trp Ala Ser Ala Asn Ser Gly Ser Gly Gly Ser Arg Gly Lys Phe Val
    690                 695                 700

Ser Gly Gly Ser Gly Arg Gly Arg His Val Arg Ser Phe Thr Arg
705                 710                 715
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<210> 5
<211> 2054
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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20 25 30

Thr Ser Ala Leu Leu Leu Ser Trp Ala Pro Ala Leu Pro Glu Ser Cys
35 40 45

Pro Gln Ile Arg His Thr Ser Val Ala Leu Leu Trp Phe Thr Phe Thr
50 55 60

Glu His Lys Ala Val Leu Asp Pro Asn Arg His Pro Ala Leu His Gly
65 70 75 80

Gly Ser Leu Gly Leu Ile Gly Thr Pro Cys Thr Ser Gly Cys Gly Gly
85 90 95

Ser Arg Val Pro Pro Ser Gly Pro Ser Ser Phe Thr Pro Ser Pro Pro
100 105 110

Ala Val Ala Lys Gly
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<210> 7

<211> 724
<212> DNA
<213> Homo sapiens

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<210> 8
<211> 128
<212> PRT
<213> Homo sapiens

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Thr Arg Ala Leu Trp Cys Phe Leu Ala Phe Arg Arg Glu Trp Gly Ile
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Gln Thr Ser Gly Leu Pro Ser Pro Trp Glu Gly Trp Gln Val Leu Gly
35 40 45

Ala Arg Pro Val Leu Arg Ala Arg Ala Leu Gly Leu Pro Pro Pro Val
50 55 60

Pro Cys Ser Thr Pro Ser Val His Lys Ala Leu Pro Ser Trp Asp Leu
65 70 75 80

Phe Arg Asp Pro Arg Asp Ala Asn Trp Pro Gly Ile Arg Ile Pro His
85 90 95

Leu Ser Lys Gln Thr Glu Ser Gly Glu Ala Pro Ser Trp Thr Ser Ser
100 105 110

Arg Cys Ser Trp Gln Arg Pro Leu Leu Leu Val Cys Ala Gln Arg Pro
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<211> 2685
<212> DNA
<213> Homo sapiens

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<210> 10
<211> 103
<212> PRT
<213> Homo sapiens

<400> 10
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1 5 10 15

Thr Pro Leu His Ser Leu Ser Trp Ser Leu Ile Ser Met Ser Ser Arg
20 25 30

Arg Val Lys Lys Gly Thr Lys Ser Arg Ser Phe Lys Pro His Pro His
35 40 45

Leu Arg Met Asp Gly Phe Leu Cys Arg Pro Cys Arg Pro Leu Ser Gln
50 55 60

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Gln Thr Phe Pro Ala Ala Leu Glu Pro Ser Lys Thr Ser Thr Thr Ser
 65                  70                  75                  80

His Gln Trp Leu Val Arg Gln Cys Pro Gln Gly Ser Cys Cys Met Pro
                85                  90                  95

Leu Ile Arg Pro Ser Trp Leu
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<210> 11
<211> 1760
<212> DNA
<213> Homo sapiens

<400> 11

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<210> 12
<211> 371
<212> PRT
<213> Homo sapiens

<400> 12

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Pro Met Glu Glu Asp Gly Leu Arg Trp Thr Pro Lys Ser Pro Leu Asp
             20                  25                  30

Pro Asp Ser Gly Leu Leu Ser Cys Thr Leu Pro Asn Gly Phe Gly Gly
```

```
        35                  40                  45

Gln Ser Gly Pro Glu Gly Glu Arg Ser Leu Ala Pro Pro Asp Ala Ser
     50                  55                  60

Ile Leu Ile Ser Asn Val Cys Ser Ile Gly Asp His Val Ala Gln Glu
 65                  70                  75                  80

Leu Phe Gln Gly Ser Asp Leu Gly Met Ala Glu Glu Ala Glu Arg Pro
                85                  90                  95

Gly Glu Lys Ala Gly Gln His Ser Pro Leu Arg Glu Glu His Val Thr
            100                 105                 110

Cys Val Gln Ser Ile Leu Asp Glu Phe Leu Gln Thr Tyr Gly Ser Leu
        115                 120                 125

Ile Pro Leu Ser Thr Asp Glu Val Val Glu Lys Leu Glu Asp Ile Phe
    130                 135                 140

Gln Gln Glu Phe Ser Thr Pro Ser Arg Lys Gly Leu Val Leu Gln Leu
145                 150                 155                 160

Ile Gln Ser Tyr Gln Arg Met Pro Gly Asn Ala Met Val Arg Gly Phe
                165                 170                 175

Arg Val Ala Tyr Lys Arg His Val Leu Thr Met Asp Asp Leu Gly Thr
            180                 185                 190

Leu Tyr Gly Gln Asn Trp Leu Asn Asp Gln Val Met Asn Met Tyr Gly
        195                 200                 205

Asp Leu Val Met Asp Thr Val Pro Glu Lys Val His Phe Phe Asn Ser
    210                 215                 220

Phe Phe Tyr Asp Lys Leu Arg Thr Lys Gly Tyr Asp Gly Val Lys Arg
225                 230                 235                 240

Trp Thr Lys Asn Val Asp Ile Phe Asn Lys Glu Leu Leu Leu Ile Pro
                245                 250                 255

Ile His Leu Glu Val His Trp Ser Leu Ile Ser Val Asp Val Arg Arg
            260                 265                 270

Arg Thr Ile Thr Tyr Phe Asp Ser Gln Arg Thr Leu Asn Arg Arg Cys
        275                 280                 285

Pro Lys His Ile Ala Lys Tyr Leu Gln Ala Glu Ala Val Lys Lys Asp
    290                 295                 300

Arg Leu Asp Phe His Gln Gly Trp Lys Gly Tyr Phe Lys Met Asn Val
305                 310                 315                 320

Ala Arg Gln Asn Asn Asp Ser Asp Cys Gly Ala Phe Val Leu Gln Tyr
                325                 330                 335

Cys Lys His Leu Ala Leu Ser Gln Pro Phe Ser Phe Thr Gln Gln Asp
            340                 345                 350

Met Pro Lys Leu Arg Arg Gln Ile Tyr Lys Glu Leu Cys His Cys Lys
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Leu Thr Val
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<210> 13
<211> 1299
<212> DNA
<213> Homo sapiens

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<211> 85
<212> PRT
<213> Homo sapiens

<400> 14
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Pro Gly Met Ser Lys Leu Cys Cys Ser Gly Ala Ser Cys His Leu Leu
20 25 30

Gly Leu Ile Pro His Leu Ile Pro Tyr Arg Glu Lys Cys Glu Phe Arg
35 40 45

Trp Arg Val Gly Pro Gly Pro Met Arg His Gln Trp Lys His Ser Ser
50 55 60

Lys Phe Arg Gln Val Pro Leu Glu Arg Lys Thr Met Thr Gly Lys Cys
65 70 75 80

Ile Ser Ser Gly Val
85

<210> 15
<211> 2996
<212> DNA
<213> Homo sapiens

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<210> 16
<211> 441
<212> PRT

<213> Homo sapiens

<400> 16

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Met Lys Leu Ala Leu Leu Leu Pro Trp Ala Cys Cys Cys Leu Cys Gly
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Ser Ala Leu Ala Thr Gly Phe Leu Tyr Pro Phe Ser Ala Ala Ala Leu
             20                  25                  30

Gln Gln His Gly Tyr Pro Glu Pro Gly Ala Gly Ser Pro Gly Ser Gly
         35                  40                  45

Tyr Ala Ser Arg Arg His Trp Cys His His Thr Val Thr Arg Thr Val
     50                  55                  60

Ser Cys Gln Val Gln Asn Gly Ser Glu Thr Val Val Gln Arg Val Tyr
 65                  70                  75                  80

Gln Ser Cys Arg Trp Pro Gly Pro Cys Ala Asn Leu Val Ser Tyr Arg
                 85                  90                  95

Thr Leu Ile Arg Pro Thr Tyr Arg Val Ser Tyr Arg Thr Val Thr Val
            100                 105                 110

Leu Glu Trp Arg Cys Cys Pro Gly Phe Thr Gly Ser Asn Cys Asp Glu
        115                 120                 125

Glu Cys Met Asn Cys Thr Arg Leu Ser Asp Met Ser Glu Arg Leu Thr
    130                 135                 140

Thr Leu Glu Ala Lys Val Leu Leu Leu Glu Ala Ala Glu Arg Pro Ser
145                 150                 155                 160

Ser Pro Asp Asn Asp Leu Pro Ala Pro Glu Ser Thr Pro Pro Thr Trp
                165                 170                 175

Asn Glu Asp Phe Leu Pro Asp Ala Ile Pro Leu Ala His Pro Val Pro
            180                 185                 190

Arg Gln Arg Arg Pro Thr Gly Pro Ala Gly Pro Pro Gly Gln Thr Gly
        195                 200                 205

Pro Pro Gly Pro Ala Gly Pro Pro Gly Ser Lys Gly Asp Arg Gly Gln
    210                 215                 220

Thr Gly Glu Lys Gly Pro Ala Gly Pro Pro Gly Leu Leu Gly Pro Pro
225                 230                 235                 240

Gly Pro Arg Gly Leu Pro Gly Glu Met Gly Arg Pro Gly Pro Pro Gly
                245                 250                 255

Pro Pro Gly Pro Ala Gly Asn Pro Gly Pro Ser Pro Asn Ser Pro Gln
            260                 265                 270

Gly Ala Leu Tyr Ser Leu Gln Pro Pro Thr Asp Lys Asp Asn Gly Asp
        275                 280                 285

Ser Arg Leu Ala Ser Ala Ile Val Asp Thr Val Leu Ala Gly Val Pro
    290                 295                 300
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Gly Pro Arg Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Arg Gly
305                 310                 315                 320

Pro Pro Gly Pro Pro Gly Thr Pro Gly Ser Gln Gly Leu Ala Gly Glu
                325                 330                 335

Arg Gly Thr Val Gly Pro Ser Gly Glu Pro Gly Val Lys Gly Glu Glu
            340                 345                 350

Gly Glu Lys Ala Ala Thr Ala Glu Gly Glu Gly Val Gln Gln Leu Arg
        355                 360                 365

Glu Ala Leu Lys Ile Leu Ala Glu Arg Val Leu Ile Leu Glu His Met
    370                 375                 380

Ile Gly Ile His Asp Pro Leu Ala Ser Pro Glu Gly Gly Ser Gly Gln
385                 390                 395                 400

Asp Ala Ala Leu Arg Ala Asn Leu Lys Met Lys Arg Gly Gly Ala Gln
                405                 410                 415

Pro Asp Gly Val Leu Ala Ala Leu Leu Gly Pro Asp Pro Gly Gln Lys
            420                 425                 430

Ser Val Asp Gln Ala Ser Ser Arg Lys
        435                 440
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<210> 17
<211> 850
<212> DNA
<213> Homo sapiens

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<210> 18
<211> 102
<212> PRT
<213> Homo sapiens

<400> 18
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Met Ser Asn Thr Thr Val Pro Asn Ala Pro Gln Ala Asn Ser Asp Ser
  1               5                  10                  15

Met Val Gly Tyr Val Leu Gly Pro Phe Phe Leu Ile Thr Leu Val Gly
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20 25 30

Val Val Val Ala Val Val Met Tyr Val Gln Lys Lys Lys Arg Val Asp
35 40 45

Arg Leu Arg His His Leu Leu Pro Met Tyr Ser Tyr Asp Pro Ala Glu
50 55 60

Glu Leu His Glu Ala Glu Gln Glu Leu Leu Ser Asp Met Gly Asp Pro
65 70 75 80

Lys Val Val His Gly Trp Gln Ser Gly Tyr Gln His Lys Arg Met Pro
85 90 95

Leu Leu Asp Val Lys Thr
100

<210> 19
<211> 1108
<212> DNA
<213> Homo sapiens

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<210> 20
<211> 224
<212> PRT
<213> Homo sapiens

<400> 20
Met Ala Leu Ala Ala Leu Met Ile Ala Leu Gly Ser Leu Gly Leu His
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Thr Trp Gln Ala Gln Ala Val Pro Thr Ile Leu Pro Leu Gly Leu Ala
20 25 30

Pro Asp Thr Phe Asp Asp Thr Tyr Val Gly Cys Ala Glu Glu Met Glu
35 40 45

Glu Lys Ala Ala Pro Leu Leu Lys Glu Glu Met Ala His His Ala Leu

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     50                  55                  60

Leu Arg Glu Ser Trp Glu Ala Ala Gln Glu Thr Trp Glu Asp Lys Arg
 65                  70                  75                  80

Arg Gly Leu Thr Leu Pro Pro Gly Phe Lys Ala Gln Asn Gly Ile Ala
                85                  90                  95

Ile Met Val Tyr Thr Asn Ser Ser Asn Thr Leu Tyr Trp Glu Leu Asn
            100                 105                 110

Gln Ala Val Arg Thr Gly Gly Gly Ser Arg Glu Leu Tyr Met Arg His
        115                 120                 125

Phe Pro Phe Lys Ala Leu His Phe Tyr Leu Ile Arg Ala Leu Gln Leu
    130                 135                 140

Leu Arg Gly Ser Gly Gly Cys Ser Arg Gly Pro Gly Glu Val Val Phe
145                 150                 155                 160

Arg Gly Val Gly Ser Leu Arg Phe Glu Pro Lys Arg Leu Gly Asp Ser
                165                 170                 175

Val Arg Leu Gly Gln Phe Ala Ser Ser Ser Leu Asp Lys Ala Val Ala
            180                 185                 190

His Arg Phe Gly Glu Lys Arg Arg Gly Cys Val Ser Ala Pro Gly Ala
        195                 200                 205

Leu Gly Thr Gly Asp Leu His Met Thr Lys Arg His Leu Gln Gln Pro
    210                 215                 220
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<210> 21
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<212> DNA
<213> Homo sapiens

<400> 21

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<210> 22
<211> 148
<212> PRT
<213> Homo sapiens

<400> 22
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20 25 30

Arg Arg Glu Arg Gly Val Ser Pro Arg Pro Gly Ala Gly Lys Glu Cys
35 40 45

Val Ala Gln Leu Ser Ala Leu Leu Ile Leu Ile Met Glu Lys Pro Leu
50 55 60

Phe Leu Ser Pro Phe Pro Glu Leu Val Phe Cys Cys Phe Cys Phe Ile
65 70 75 80

Leu Phe Trp Gly Asp Ser Phe Leu Leu Phe Asn Leu Glu Ser Pro Val
85 90 95

Pro Leu Gly Cys Arg Gln Phe Leu Pro Gly Pro Ser Arg Asn Pro His
100 105 110

Ser Pro Ser Pro Leu Leu Arg Tyr Leu Gln Glu Ala Ala Asn Leu Val
115 120 125

His Ser Asp Lys Pro Pro Thr Gln Ile Ser Leu Leu Pro Leu Cys Pro
130 135 140

Lys Ser His His
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<210> 23
<211> 2538
<212> DNA
<213> Homo sapiens

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His Leu Leu His Gly Tyr Ile Lys Leu Leu Thr Val Ser Thr Leu Ser
35 40 45

Cys Tyr Leu Gln Asn Trp Asp Asn Met Ile Pro Ser Val Ala Ile Val
50 55 60

Phe Leu Ile Trp Pro Arg Asp Leu Leu Lys Leu Asp Met Gly Gly Asn
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Leu Phe Cys Phe Gly Ile Gln Lys Gly Asn Ile Cys Lys Thr Val Leu
85 90 95

Lys Asp Gln Lys Ser Cys Ser Tyr Phe Asp Cys Tyr Asn Leu Leu Ile
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<211> 125
<212> PRT
<213> Homo sapiens

<400> 26
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Cys Glu Arg Gly Arg Cys Ser Ala Ala Ser Trp Pro Leu Arg Ala Arg
20 25 30

Gly Leu Ala Gln Cys Ile Gln Leu Pro Thr Gly Leu Val Gln Arg Gln
35 40 45

Pro Cys Leu Pro Glu His Gly Ile Phe Lys Asn Pro Pro Ala Leu Gly
50 55 60

Ser Val Cys Ser His Pro Gly Ser Ile Arg Ser Leu Leu Cys Arg Arg
65 70 75 80

Asn Ala His Thr Thr Ala Leu Pro Leu Phe Glu Asp Leu Pro Ser Cys
85 90 95

Leu Ser Arg Arg Val Pro Arg Gly Asp Leu Pro Ser Val Leu Pro Gly
100 105 110

Ala Leu Val Ala His Leu Ala Val Leu Pro Leu Thr Cys
115 120 125

<210> 27
<211> 2667

<212> DNA
<213> Homo sapiens

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<210> 28
<211> 232
<212> PRT
<213> Homo sapiens

<400> 28
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Ala Arg Gly Ala Leu Gly Trp Gly Leu Cys Met Cys Leu Lys Val Ala

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Ala Val Arg His Ser Phe Ser Pro Pro Pro His Pro Thr Gly Arg Ala
        35                  40                  45

Ala Arg Arg Pro Cys Gly Ser Asp Ser Arg Trp Cys Pro Trp Pro Pro
    50                  55                  60

Cys Gly Ser Pro Ala Cys Cys Gly Ser Thr Cys Pro Ala Ser Gly Ser
65                  70                  75                  80

Thr Ser Ser Thr Pro Ser Gln Ser Gln Ala Pro Ser Pro Thr Arg Pro
                85                  90                  95

Ser Ser Ala Pro Thr Glu Val Arg Arg Pro Leu Trp Trp Glu Ser Arg
            100                 105                 110

Val Gly Ser Trp Ala Glu Pro Gln Leu Arg Ser Leu Tyr Leu Leu Pro
        115                 120                 125

Arg His Pro Ala Pro Gln Ile Pro Leu His Arg Arg Pro Gly Gly His
    130                 135                 140

Pro Ala Pro Glu Arg Leu Gly Ala Pro Val Gln Gln Ile Arg Gly Trp
145                 150                 155                 160

Pro Arg Arg Glu Pro Pro Val Arg Val Leu His Leu Pro Gly Gly Asp
                165                 170                 175

Arg Gly Thr Gly Gln Ala Gln Glu Asp Arg Asp Arg His Leu His Gln
            180                 185                 190

Val Glu Gln Gly Leu Pro Gly Arg Gly Val Ala Gly Arg His Leu Leu
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His Gln His Ala Val Val Pro Gly Val Gly Gly Val Arg Gln Gly Glu
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Gly Gln Arg Ala Pro Arg Ala His
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<210> 29
<211> 2699
<212> DNA
<213> Homo sapiens

<400> 29

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<210> 30
<211> 166
<212> PRT
<213> Homo sapiens

<400> 30

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             20                  25                  30

Leu Phe Tyr Phe Gly Leu Ile Ser Leu Lys Val Leu Asn Ser Ile Val
         35                  40                  45

Leu Leu Gly Lys Ser Cys Gln Tyr Val Lys Glu Ala Lys Met Glu Glu
     50                  55                  60

Lys Leu Ser Asn Pro Pro Ala Thr Cys Thr Pro Gly Lys Pro Ser Ser
 65                  70                  75                  80

Lys Ser Gln Asn Lys Cys Lys Pro Ser Gln Gly Leu Ser Thr Glu Glu
                 85                  90                  95

Asn Leu Ser Ala Ser Ile Thr Lys Gln Pro Ile His Gln Lys Glu Asn
            100                 105                 110
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Ile Ile Pro Leu Leu Val Thr Ser Asn Ser Asp Gln Phe Leu Thr Thr
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Pro Asp Gly Asp Glu Lys Asp Ile Thr Gln Asp Asn Ser Glu Leu Lys
    130                 135                 140

His Arg Ser Ser Lys Lys Asp Leu Leu Glu Ile Asp Arg Phe Thr Ile
145                 150                 155                 160

Cys Gly Asn Arg Ile Asp
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<210> 31
<211> 1300
<212> DNA
<213> Homo sapiens

<400> 31
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<210> 32
<211> 145
<212> PRT
<213> Homo sapiens

<400> 32
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Met Ile Pro Ile Trp Lys Gln Gln Ala Arg Pro Gly Asp Gly Pro Val
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Ile Trp Asp Tyr His Val Val Leu Leu His Val Ser Ser Gly Gly Gln
             20                  25                  30

Ser Phe Ile Tyr Asp Leu Asp Thr Val Leu Pro Phe Pro Cys Leu Phe
         35                  40                  45

Asp Thr Tyr Val Glu Asp Ala Ile Lys Ser Asp Asp Asp Ile His Pro
     50                  55                  60
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Gln Phe Arg Arg Lys Phe Arg Val Ile Cys Ala Asp Ser Tyr Leu Lys
 65                  70                  75                  80

Asn Phe Ala Ser Asp Arg Ser His Met Lys Asp Ser Ser Gly Asn Trp
                85                  90                  95

Arg Glu Pro Pro Pro Pro Tyr Pro Cys Ile Glu Thr Gly Asp Ser Lys
            100                 105                 110

Met Asn Leu Asn Asp Phe Ile Ser Met Asp Pro Lys Val Gly Trp Gly
        115                 120                 125

Ala Val Tyr Thr Leu Ser Glu Phe Thr His Arg Phe Gly Ser Lys Asn
    130                 135                 140

Cys
145
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<210> 33
<211> 1256
<212> DNA
<213> Homo sapiens

<400> 33
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<210> 34
<211> 189
<212> PRT
<213> Homo sapiens

<400> 34
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Met Thr Leu Ala Ala Tyr Lys Glu Lys Met Lys Glu Leu Pro Leu Val
  1               5                  10                  15

Ser Leu Phe Cys Ser Cys Phe Leu Ala Asp Pro Leu Asn Lys Ser Ser
             20                  25                  30
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Tyr Lys Tyr Glu Ala Asp Thr Val Asp Leu Asn Trp Cys Val Ile Ser
         35                  40                  45

Asp Met Glu Val Ile Glu Leu Asn Lys Cys Thr Ser Gly Gln Ser Phe
     50                  55                  60

Glu Val Ile Leu Lys Pro Pro Ser Phe Asp Gly Val Pro Glu Phe Asn
 65                  70                  75                  80

Ala Ser Leu Pro Arg Arg Arg Asp Pro Ser Leu Glu Glu Ile Gln Lys
                 85                  90                  95

Lys Leu Glu Ala Ala Glu Glu Arg Arg Lys Tyr Gln Glu Ala Glu Leu
            100                 105                 110

Leu Lys His Leu Ala Glu Lys Arg Glu His Glu Arg Glu Val Ile Gln
        115                 120                 125

Lys Ala Ile Glu Glu Asn Asn Asn Phe Ile Lys Met Ala Lys Glu Lys
    130                 135                 140

Leu Ala Gln Lys Met Glu Ser Asn Lys Glu Asn Arg Glu Ala His Leu
145                 150                 155                 160

Ala Ala Met Leu Glu Arg Leu Gln Glu Lys Asp Lys His Ala Glu Glu
                165                 170                 175

Val Arg Lys Asn Lys Glu Leu Lys Glu Glu Ala Ser Arg
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<210> 35
<211> 1783
<212> DNA
<213> Homo sapiens

<400> 35

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<210> 36
<211> 116
<212> PRT
<213> Homo sapiens

<400> 36
Met Ala Ser Ser Ser Asp Gly Ile Ser Leu Ser Tyr Arg Pro Val Val
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Thr Gly Gln Asp Arg Met Met Asp Thr Glu Val Leu Ser Leu Leu Ser
20 25 30

Ser Val Ala Leu Pro Ser Leu Leu Leu Ala Ser Glu Ser Phe Asp Ser
35 40 45

Ile Tyr Pro Gly Ile Phe Cys Val Leu Met Phe Ser Ser Gly Leu Val
50 55 60

Ser Ala Val Leu Ile Gly Arg Ala Leu Ser Phe Gln Ala Ile Leu Lys
65 70 75 80

Gly Gly Gln Ser Lys Gly Gln Ser Leu Asn Pro Phe Cys Gly Leu Asn
85 90 95

Asn Leu Arg Ile Lys Ser Ser Val Leu Leu Ile Pro Val Leu Leu Cys
100 105 110

Gln Thr Leu Ser
115

<210> 37
<211> 1725
<212> DNA
<213> Homo sapiens

<400> 37
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<210> 38
<211> 74
<212> PRT
<213> Homo sapiens

<400> 38
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Ser Ser Leu Val Thr Trp Gly Cys Gln Ala Gly Phe Trp Lys Thr Ser
20 25 30

Ala Leu Lys Leu Ile Leu Lys Arg Ala Val Pro Ala Leu Trp Pro Pro
35 40 45

Gly Gly Pro Asp Ser Pro Glu Thr Thr Phe Cys Pro Lys Asn Met Leu
50 55 60

Ser Ile Trp Gly Ile Ser Ser His Lys Pro
65 70

<210> 39
<211> 1953
<212> DNA
<213> Homo sapiens

<400> 39
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gctggatata ttatatgcaa ttaatagtag ttaagaattt attcatttgg tagatatgtt 1860
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<210> 40
<211> 463
<212> PRT
<213> Homo sapiens

<400> 40
Met Ala Leu Ser Cys Thr Leu Asn Arg Tyr Leu Leu Leu Met Ala Gln
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Glu His Leu Glu Phe Arg Leu Pro Glu Ile Lys Ser Leu Leu Leu Leu
20 25 30

Phe Gly Gly Gln Phe Ala Ser Ser Gln Glu Thr Tyr Gly Lys Ser Pro
35 40 45

Phe Trp Ile Leu Ser Ile Pro Ser Glu Asp Ile Ala Arg Asn Leu Met
50 55 60

Lys Arg Thr Val Cys Ala Lys Ser Ile Phe Glu Leu Trp Gly His Gly
65 70 75 80

Gln Ser Pro Glu Glu Leu Tyr Ser Ser Leu Lys Asn Tyr Pro Val Glu
85 90 95

Lys Met Val Pro Phe Leu His Ser Asp Ser Thr Tyr Lys Ile Lys Ile
100 105 110

His Thr Phe Asn Lys Thr Leu Thr Gln Glu Glu Lys Ile Lys Arg Ile
115 120 125

Asp Ala Leu Glu Phe Leu Pro Phe Glu Gly Lys Val Asn Leu Lys Lys
130 135 140

Pro Gln His Val Phe Ser Val Leu Glu Asp Tyr Gly Leu Asp Pro Asn
145 150 155 160

Cys Ile Pro Glu Asn Pro His Asn Ile Tyr Phe Gly Arg Trp Ile Ala
165 170 175

Asp Gly Gln Arg Glu Leu Ile Glu Ser Tyr Ser Val Lys Lys Arg His
180 185 190

Phe Ile Gly Asn Thr Ser Met Asp Ala Gly Leu Ser Phe Ile Met Ala

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        195                 200                 205

Asn His Gly Lys Val Lys Glu Asn Asp Ile Val Phe Asp Pro Phe Val
    210                 215                 220

Gly Thr Gly Gly Leu Leu Ile Ala Cys Ala His Phe Gly Ala Tyr Val
225                 230                 235                 240

Tyr Gly Thr Asp Ile Asp Tyr Asn Thr Val His Gly Leu Gly Lys Ala
                245                 250                 255

Thr Arg Lys Asn Gln Lys Trp Arg Gly Pro Asp Glu Asn Ile Arg Ala
            260                 265                 270

Asn Leu Arg Gln Tyr Gly Leu Glu Lys Tyr Tyr Leu Asp Val Leu Val
        275                 280                 285

Ser Asp Ala Ser Lys Pro Ser Trp Arg Lys Gly Thr Tyr Phe Asp Ala
    290                 295                 300

Ile Ile Thr Asp Pro Pro Tyr Gly Ile Arg Glu Ser Thr Arg Arg Thr
305                 310                 315                 320

Gly Ser Gln Lys Glu Ile Pro Lys Gly Ile Glu Lys Trp Glu Lys Cys
                325                 330                 335

Pro Glu Ser His Val Pro Val Ser Leu Ser Tyr His Leu Ser Asp Met
            340                 345                 350

Phe Leu Asp Leu Leu Asn Phe Ala Ala Glu Thr Leu Val Leu Gly Gly
        355                 360                 365

Arg Leu Val Tyr Trp Leu Pro Val Tyr Thr Pro Glu Tyr Thr Glu Glu
    370                 375                 380

Met Val Pro Trp His Pro Cys Leu Glu Leu Val Ser Asn Cys Glu Gln
385                 390                 395                 400

Lys Leu Ser Ser His Thr Ser Arg Arg Leu Ile Thr Met Glu Lys Val
                405                 410                 415

Lys Lys Phe Glu Asn Arg Asp Gln Tyr Ser His Leu Leu Ser Asp His
            420                 425                 430

Phe Leu Pro Tyr Gln Gly His Asn Ser Phe Arg Glu Lys Tyr Phe Ser
        435                 440                 445

Gly Val Thr Lys Arg Ile Ala Lys Glu Glu Lys Ser Thr Gln Glu
    450                 455                 460
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<210> 41
<211> 1605
<212> DNA
<213> Homo sapiens

<400> 41
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atttgatttg aggtgaggta aaagcctgaa acatggaatg gcattctgtt ttgatggatt 180

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<210> 42
<211> 87
<212> PRT
<213> Homo sapiens

<400> 42
Met Glu Trp His Ser Val Leu Met Asp Phe His Phe Phe Ala Leu Leu
1 5 10 15

Arg Arg Gln Ser Gln Pro Leu Arg Ser Leu Pro His Leu Cys His Leu
20 25 30

Pro Gly Ser Cys Ser Leu Met Tyr Leu Trp Val Val Arg Trp Lys Trp
35 40 45

Cys Leu Gln Lys Leu Gly Arg Arg Ile Leu Leu His Ser Leu His Asp
50 55 60

Val Phe Ile Ala Asn Met Asp Asp Lys Gly Leu Cys Tyr Arg Gly Leu
65 70 75 80

Arg Ala Pro Ser Phe Leu Leu
85

<210> 43
<211> 1936
<212> DNA
<213> Homo sapiens

<400> 43
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gactgcctct cttcctgttc ccaggggcct gggcccaggg ccatgtccca cccggctgca 180
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cagagtggct gatcatcacc ctggttcggg gcagtggcga gggcggccct cagggcaaca 660
gcagcgcagg ctgggccgtg gcctcccct gtgccatcgc caacatggac tttgtcatgg 720
cactcatcta cgtcatgctg ctgctgctgg gtgccttcct gggggcctgg cccgccctgt 780
gtggccgcta caagcgctgg cgtaagcatg gggtctttgt gctcctcacc acagccacct 840
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gtcccacctg ggatgacccc acgctggcca tcgccctcgc cgccaatgcc tgggccttcg 960
tcctcttcta cgtcatcccc gaggtctccc aggtgaccaa gtccagccca gagcaaagct 1020
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agggtcagag catgttcgtg gagaacaagg ccttttccat ggatgagccg gttgcagcta 1140
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atttggggag ggccctgagg acctggcccc gggcaaggga ctctccaggc tcctcctccc 1500
cctggcaggc ccagcaacat gtgccccaga tgtggaaggg cctccctctc tgccagtgtt 1560
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aggcgctcag gcctggatct tgctcctctg tgaggaacaa gggtgcctaa taaatacatt 1800
tctgctttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1860
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<210> 44
<211> 441
<212> PRT
<213> Homo sapiens

<400> 44

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Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe
  1               5                  10                  15

Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser
             20                  25                  30

Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala
         35                  40                  45

Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr
     50                  55                  60

Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp
 65                  70                  75                  80

Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly
                 85                  90                  95

Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp
            100                 105                 110

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala
        115                 120                 125
```

```
Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu
    130                 135                 140

Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala
145                 150                 155                 160

Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile
                165                 170                 175

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser
            180                 185                 190

Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp
        195                 200                 205

Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe
    210                 215                 220

Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys
225                 230                 235                 240

His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp
                245                 250                 255

Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser
            260                 265                 270

Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala
        275                 280                 285

Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr
    290                 295                 300

Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg
305                 310                 315                 320

Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met
                325                 330                 335

Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys
            340                 345                 350

Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser
        355                 360                 365

Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu
    370                 375                 380

Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val
385                 390                 395                 400

Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala
                405                 410                 415

Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln
            420                 425                 430

Val Phe Arg Asn Pro Tyr Val Trp Asp
        435                 440
```

<210> 45
<211> 1773
<212> DNA
<213> Homo sapiens

<400> 45
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cgatgtacgt gactctcgtg ttccgcgtga agggctcccg cctggtcaaa ccctcgctct 120
gcctggcctt gctgtgcccg gccttcctgg tgggcgtggt ccgcgtggcc gagtaccgaa 180
accactggtc ggacgtgctg gctggcttcc tgacaggggc ggccatcgcc acctttttgg 240
tcacctgcgt tgtgcataac tttcagagcc ggccaccctc tggccgaagg ctctctccct 300
gggaggacct gggccaagcc cccaccatgg atagcccccc cgaaaagaac ccgaggtctg 360
caggccgcat tcgacaccgg cacggctcac cccatccaag tcgcagaact gcgcccgccg 420
tggccacctg atccccagct gtgtctcctc cagggcccca gccatgtgtt cgtcgccccg 480
tgtgccccgt cctcgattga ggtctgagcc gacgcccttg cccctgcccc taccctgcc 540
agcgcccacc cccagccagg gcccctcgcc ttcctcccct ggacctgggg ggccaggcgg 600
gggtggtgga cgtggccgga agctgctgct gcccacgccc ctgctgcggg acctgtacac 660
cctgagtgga ctctatccct ccccttccca ccgggacaac ttcagccctt acctgtttgc 720
cagccgtgac cacctgctgt gaggcccgac cacccaccca gaatctgccc agtccccact 780
tcttccctgc cacgcgtgtg tgtgcgtgtg ccacgtgagt gccaaagtcc cctgcccccc 840
aagccagcca gacccagaca ttagtaagat ggctagaagg acatttagga gacatctgcc 900
tctctggccc tctgagatat cccgatgggc acaaatggaa ggtgcgcact tgcccctact 960
attgcccttt taagggccaa agcttgaccc cattggccat tgcctggcta atgagaaccc 1020
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gaccgcccgt gtctaagcat gtgcaaagga gaggagggag atgaggtcat tgtttgtcat 1260
tgagtcttct ctcagaatca gcgagcccag ctgtagggtg gggggcaggc tcccccatgg 1320
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ctcacccact ctctcctaat cccctactta agtagggctt gccccacttc agaggttttg 1440
gggttcaggg tgctgtgtct cccccttgcct gtgcccaggt catcccaaac ccttctgtta 1500
tttattaggg ctgtgggaag ggtttttctt ctttttcttg gaacctgccc ctgttcttca 1560
cactgccccc catgcctcag cctcatacag atgtgccatc atgggggggca tgggtggagc 1620
agaggggctc cctcaccccg ggcaggcaaa ggcagtgggt agaggaggca ctgccccccct 1680
ttcctgcccc ctcctcatct ttaataaaga cctggcttct catctttaat aaagacctgt 1740
ttgtaacaga aaaaaaaaaa aaaaaaaaaa aaa 1773

<210> 46
<211> 122
<212> PRT
<213> Homo sapiens

<400> 46
Met Tyr Val Thr Leu Val Phe Arg Val Lys Gly Ser Arg Leu Val Lys
1 5 10 15

Pro Ser Leu Cys Leu Ala Leu Leu Cys Pro Ala Phe Leu Val Gly Val
20 25 30

Val Arg Val Ala Glu Tyr Arg Asn His Trp Ser Asp Val Leu Ala Gly
35 40 45

Phe Leu Thr Gly Ala Ala Ile Ala Thr Phe Leu Val Thr Cys Val Val
50 55 60

His Asn Phe Gln Ser Arg Pro Pro Ser Gly Arg Arg Leu Ser Pro Trp
65 70 75 80

Glu Asp Leu Gly Gln Ala Pro Thr Met Asp Ser Pro Leu Glu Lys Asn

85 90 95

Pro Arg Ser Ala Gly Arg Ile Arg His Arg His Gly Ser Pro His Pro
100 105 110

Ser Arg Arg Thr Ala Pro Ala Val Ala Thr
115 120

<210> 47
<211> 1974
<212> DNA
<213> Homo sapiens

<400> 47
tctgcatcct tcccgacctt cccagcaata tgcatcttgc acgtctggtc ggctcctgct 60
ccctccttct gctactgggg gccctgtctg gatgggcggc cagcgatgac cccattgaga 120
aggtcattga agggatcaac cgagggctga gcaatgcaga gagagaggtg ggcaaggccc 180
tggatggcat caacagtgga atcacgcatg ccggaaggga agtggagaag gttttcaacg 240
gacttagcaa catggggagc cacaccggca aggagttgga caaaggcgtc caggggctca 300
accacggcat ggacaaggtt gcccatgaga tcaaccatgg tattggacaa gcaggaaagg 360
aagcagagaa gcttggccat ggggtcaaca acgctgctgg acaggttggg aaggaggcag 420
acaaactgat ccatcatggg gtccatcacg gggccaacca ggcgggaagt gaggcaggga 480
agtttggcca gggagtcgac aatgctgcag ggcaggctgg aaatgaggct gggaggtttg 540
gccagggagt ccaccatgct gcagggcagg ccggaaatga ggctgggagg tttggccagg 600
gagtccacca tgctgcaggg caggccggaa atgaggctgg gagatttggc caggggccc 660
accatggtct cagtgagggc tggaaggaga cagagaagtt tggccagggg atccaccatg 720
ctgccggtca ggttgggaag gaggcagaga agtttggcca gggggcccac catgctgcgg 780
ggcaggccgg aaatgaggca gggagatttg gccaggggt ccaccatggt ctcagtgagg 840
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aggaggcaga gaagtttggc caggggccc accatgctgc ggggcaggcc ggaaatgagg 960
cagggagatt tggccagggg gcccaccatg ctgcggggca ggccggaaat gaggctggga 1020
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gccaggggt ccaccatgct gccagtcagt ttgggaagga aacagagaag ctcggccatg 1140
gggtccacca tggggttaat gaggcctgga aggaagcaga gaagtttggc cagggtgtcc 1200
accatgctgc ctcgcaggtg gggaaggagg aagacagagt ggtccaaggc ctccatcatg 1260
gcgttagtca ggctggaagg gaggggggc agtttggcca cgacattcac cacacagcag 1320
ggcaggctgg gaaagaggga gacatagcag ttcatggtgt ccaacctggg gtccacgagg 1380
ccgggaagga ggcagggcag tttggccagg gagttcacca tacccttgaa caggccggga 1440
aggaagcaga caaagcggtc caagggttcc acactggggt ccaccaggct gggaaggaag 1500
cagagaaact tggccaaggg gtcaaccatg ctgctgacca ggctggaaag gaagtggaga 1560
agcttggcca aggtgcccac catgctgctg gccaggccgg gaaggagctg cagaatgctc 1620
ataatggggt caaccaagcc agcaaggagg ccaaccagct gctgaatggc aaccatcaaa 1680
gcggatcttc cagccatcaa ggaggggcca caaccacgcc gttagcctct ggggcctcag 1740
tcaacacgcc tttcatcaac cttcccgccc tgtggaggag cgtcgccaac atcatgccct 1800
aaactggcat ccggccttgc tgggagaata atgtcgccgt tgtcacatca gctgacatga 1860
cctggagggg ttgggggtgg gggacaggtt tctgaaatcc ctgaaggggg ttgtactggg 1920
atttgtgaat aaacttgata cactatgctg tcaaaaaaaa aaaaaaaaaa aaaa 1974

<210> 48
<211> 590
<212> PRT
<213> Homo sapiens

<400> 48
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu Leu
1 5 10 15

Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
20 25 30

```
Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
         35                  40                  45

Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
     50                  55                  60

Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
 65                  70                  75                  80

Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
                 85                  90                  95

Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
            100                 105                 110

Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Val Gly Lys
        115                 120                 125

Glu Ala Asp Lys Leu Ile His His Gly Val His His Gly Ala Asn Gln
    130                 135                 140

Ala Gly Ser Glu Ala Gly Lys Phe Gly Gln Gly Val Asp Asn Ala Ala
145                 150                 155                 160

Gly Gln Ala Gly Asn Glu Ala Gly Arg Phe Gly Gln Gly Val His His
                165                 170                 175

Ala Ala Gly Gln Ala Gly Asn Glu Ala Gly Arg Phe Gly Gln Gly Val
            180                 185                 190

His His Ala Ala Gly Gln Ala Gly Asn Glu Ala Gly Arg Phe Gly Gln
        195                 200                 205

Gly Ala His His Gly Leu Ser Glu Gly Trp Lys Glu Thr Glu Lys Phe
    210                 215                 220

Gly Gln Gly Ile His His Ala Ala Gly Gln Val Gly Lys Glu Ala Glu
225                 230                 235                 240

Lys Phe Gly Gln Gly Ala His His Ala Ala Gly Gln Ala Gly Asn Glu
                245                 250                 255

Ala Gly Arg Phe Gly Gln Gly Val His His Gly Leu Ser Glu Gly Trp
            260                 265                 270

Lys Glu Thr Glu Lys Phe Gly Gln Gly Val His His Thr Ala Gly Gln
        275                 280                 285

Val Gly Lys Glu Ala Glu Lys Phe Gly Gln Gly Ala His His Ala Ala
    290                 295                 300

Gly Gln Ala Gly Asn Glu Ala Gly Arg Phe Gly Gln Gly Ala His His
305                 310                 315                 320

Ala Ala Gly Gln Ala Gly Asn Glu Ala Gly Arg Phe Gly Gln Gly Val
                325                 330                 335

His His Gly Leu Ser Glu Gly Trp Lys Glu Thr Glu Lys Phe Gly Gln
            340                 345                 350
```

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Gly Val His His Ala Ala Ser Gln Phe Gly Lys Glu Thr Glu Lys Leu
        355                 360                 365

Gly His Gly Val His His Gly Val Asn Glu Ala Trp Lys Glu Ala Glu
    370                 375                 380

Lys Phe Gly Gln Gly Val His His Ala Ala Ser Gln Val Gly Lys Glu
385                 390                 395                 400

Glu Asp Arg Val Val Gln Gly Leu His His Gly Val Ser Gln Ala Gly
                405                 410                 415

Arg Glu Gly Gly Gln Phe Gly His Asp Ile His His Thr Ala Gly Gln
            420                 425                 430

Ala Gly Lys Glu Gly Asp Ile Ala Val His Gly Val Gln Pro Gly Val
        435                 440                 445

His Glu Ala Gly Lys Glu Ala Gly Gln Phe Gly Gln Gly Val His His
    450                 455                 460

Thr Leu Glu Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln Gly Phe
465                 470                 475                 480

His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly Gln
                485                 490                 495

Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu Val Glu Lys Leu
            500                 505                 510

Gly Gln Gly Ala His His Ala Ala Gly Gln Ala Gly Lys Glu Leu Gln
        515                 520                 525

Asn Ala His Asn Gly Val Asn Gln Ala Ser Lys Glu Ala Asn Gln Leu
    530                 535                 540

Leu Asn Gly Asn His Gln Ser Gly Ser Ser Ser His Gln Gly Gly Ala
545                 550                 555                 560

Thr Thr Thr Pro Leu Ala Ser Gly Ala Ser Val Asn Thr Pro Phe Ile
                565                 570                 575

Asn Leu Pro Ala Leu Trp Arg Ser Val Ala Asn Ile Met Pro
            580                 585                 590
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<210> 49
<211> 923
<212> DNA
<213> Homo sapiens

<400> 49
gagagctgga tccttgaaaa tctactctat cagctgctgt ggttgccacc attctcagga 60
ccctcgccat gaaagccctt atgctgctca ccctgtctgt tctgctctgc tgggtctcag 120
ctgacattcg ctgtcactcc tgctacaagg tccctgtgct gggctgtgtg gaccggcagt 180
cctgccgcct ggagccagga cagcaatgcc tgacaacaca tgcatacctt ggtaagatgt 240
gggttttctc caatctgcgc tgtggcacac cagaagagcc ctgtcaggag gccttcaacc 300
aaaccaaccg taagctgggt ctgacatata acaccacctg ctgcaacaag gacaactgca 360
acagcgcagg accccggccc actccagccc tgggccttgt cttccttacc tccttggctg 420

gccttggcct ctggctgctg cactgagact cattccattg gctgcccctc ctcccacctg 480
ccttggcctg agcctctctc cctgtgtctc tgtatcccct ggctttacag aatcgtctct 540
ccctagctcc catttcttta attaaacact gttccgagtg gtctcctcat ccgtccttcc 600
cacctcacac ccttcactct ccttttctg ggtcccttcc cacttccttc caggacctcc 660
attggctcct agaagggctc cccactttgc ttcctatact ctgctgtccc ctacttgagg 720
agggattggg atctggggcc tgaaatgggg cttctgtgtt gtccccagtg aaggctccca 780
caaggacctg atgacctcac tgtacagagc tgactcccca aatccaggct cccatatgta 840
ccccatcccc catactcacc tctttccatt ttgagtaata aatgtctgag tctgaaaaaa 900
aaaaaaaaaa aaaaaaaaaa aaa 923

<210> 50
<211> 125
<212> PRT
<213> Homo sapiens

<400> 50
Met Lys Ala Leu Met Leu Leu Thr Leu Ser Val Leu Leu Cys Trp Val
1 5 10 15

Ser Ala Asp Ile Arg Cys His Ser Cys Tyr Lys Val Pro Val Leu Gly
20 25 30

Cys Val Asp Arg Gln Ser Cys Arg Leu Glu Pro Gly Gln Gln Cys Leu
35 40 45

Thr Thr His Ala Tyr Leu Gly Lys Met Trp Val Phe Ser Asn Leu Arg
50 55 60

Cys Gly Thr Pro Glu Glu Pro Cys Gln Glu Ala Phe Asn Gln Thr Asn
65 70 75 80

Arg Lys Leu Gly Leu Thr Tyr Asn Thr Thr Cys Cys Asn Lys Asp Asn
85 90 95

Cys Asn Ser Ala Gly Pro Arg Pro Thr Pro Ala Leu Gly Leu Val Phe
100 105 110

Leu Thr Ser Leu Ala Gly Leu Gly Leu Trp Leu Leu His
115 120 125

<210> 51
<211> 1493
<212> DNA
<213> Homo sapiens

<400> 51
ggagaagccc aggcagttga ggacaggaga gagaaggctg cagacccaga gggagggagg 60
acagggagtc ggaaggagga ggacagagga gggcacagag acgcagagca agggcggcaa 120
ggaggagacc ctggtgggag gaagacactc tggagagaga gggggctggg cagagatgaa 180
gttccagggg cccctggcct gcctcctgct ggccctctgc ctgggcagtg gggaggctgg 240
ccccctgcag agcggagagg aaagcactgg gacaaatatt ggggaggccc ttggacatgg 300
cctgggagac gccctgagcg aaggggtggg aaaggccatt ggcaaagagg ccggaggggc 360
agctggctct aaagtcagtg aggcccttgg ccaagggacc agagaagcag ttggcactgg 420
agtcaggcag gttccaggct ttggcgtagc agatgctttg ggcaacaggg tcggggaagc 480
agcccatgct ctgggaaaca ctgggcacga gattggcaga caggcagaag atgtcattcg 540
acacggagca gatgctgtcc gcggctcctg gcaggggtg cctggccaca atggtgcttg 600
ggaaacttct ggaggccatg gcatctttgg ctctcaaggt ggccttggag gccagggcca 660
gggcaatcct ggaggtctgg ggactccgtg ggtccacgga taccccggaa actcagcagg 720
cagctttgga atgaatcctc agggagctcc ctggggtcaa ggaggcaatg gagggccacc 780

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aaactttggg accaacactc agggagctgt ggcccagcct ggctatggtt cagtgagagc 840
cagcaaccag aatgaagggt gcacgaatcc cccaccatct ggctcaggtg gaggctccag 900
caactctggg ggaggcagcg gctcacagtc gggcagcagt ggcagtggca gcaatggtga 960
caacaacaat ggcagcagca gtggtggcag cagcagtggc agcagcagtg gcggcagcag 1020
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tgagtcctcc tggggatcca gcaccggctc ctcctccggc aaccacggtg gagcggcgga 1140
ggaaatggac ataaacccgg gaactctgag acgtctcctg ggatgtttaa ctttgacact 1200
ttctggaaga attttaaatc caagctgggt ttcatcaact gggatgccat aaacaaggac 1260
cagagaagct ctcgcatccc gtgacctcca gacaaggagc caccagattg gatgggagcc 1320
cccacactcc ctccttaaaa caccaccctc tcatcactaa tctcagccct tgcccttgaa 1380
ataaacctta gctgccccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa                    1493
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<210> 52
<211> 358
<212> PRT
<213> Homo sapiens

<400> 52

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Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu
  1               5                  10                  15

Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser Thr Gly
             20                  25                  30

Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp Ala Leu Ser
         35                  40                  45

Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly Gly Ala Ala Gly
     50                  55                  60

Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr Arg Glu Ala Val Gly
 65                  70                  75                  80

Thr Gly Val Arg Gln Val Pro Gly Phe Gly Val Ala Asp Ala Leu Gly
                 85                  90                  95

Asn Arg Val Gly Glu Ala Ala His Ala Leu Gly Asn Thr Gly His Glu
            100                 105                 110

Ile Gly Arg Gln Ala Glu Asp Val Ile Arg His Gly Ala Asp Ala Val
        115                 120                 125

Arg Gly Ser Trp Gln Gly Val Pro Gly His Asn Gly Ala Trp Glu Thr
    130                 135                 140

Ser Gly Gly His Gly Ile Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln
145                 150                 155                 160

Gly Gln Gly Asn Pro Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr
                165                 170                 175

Pro Gly Asn Ser Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro
            180                 185                 190

Trp Gly Gln Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr
        195                 200                 205

Gln Gly Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn
    210                 215                 220
```

```
Gln Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
225                 230                 235                 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser Gly
                245                 250                 255

Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly Gly Ser
            260                 265                 270

Ser Ser Gly Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly
        275                 280                 285

Ser Ser Gly Asn Ser Gly Gly Ser Arg Gly Asp Ser Gly Ser Glu Ser
    290                 295                 300

Ser Trp Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ala
305                 310                 315                 320

Ala Glu Glu Met Asp Ile Asn Pro Gly Thr Leu Arg Arg Leu Leu Gly
                325                 330                 335

Cys Leu Thr Leu Thr Leu Ser Gly Arg Ile Leu Asn Pro Ser Trp Val
            340                 345                 350

Ser Ser Thr Gly Met Pro
        355
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<210> 53
<211> 1897
<212> DNA
<213> Homo sapiens

<400> 53

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acagaggagg gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 60
agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc cctggcctgc 120
ctcctgctgg ccctctgcct gggcagtggg gaggctggcc ccctgcagag cggagaggaa 180
agcactggga caaatattgg ggaggccctt ggacatggcc tgggagacgc cctgagcgaa 240
ggggtgggaa aggccattgg caaagaggcc ggaggggcag ctggctctaa agtcagtgag 300
gcccttggcc aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 360
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<210> 54
<211> 479
<212> PRT
<213> Homo sapiens

<400> 54
Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu
1 5 10 15

Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser Thr Gly
20 25 30

Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp Ala Leu Ser
35 40 45

Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly Gly Ala Ala Gly
50 55 60

Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr Arg Glu Ala Val Gly
65 70 75 80

Thr Gly Val Arg Gln Val Pro Gly Phe Gly Val Ala Asp Ala Leu Gly
85 90 95

Asn Arg Val Gly Glu Ala Ala His Ala Leu Gly Asn Thr Gly His Glu
100 105 110

Ile Gly Arg Gln Ala Glu Asp Val Ile Arg His Gly Ala Asp Ala Val
115 120 125

Arg Gly Ser Trp Gln Gly Val Pro Gly His Asn Gly Ala Trp Glu Thr
130 135 140

Ser Gly Gly His Gly Ile Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln
145 150 155 160

Gly Gln Gly Asn Pro Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr
165 170 175

Pro Gly Asn Ser Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro
180 185 190

Trp Gly Gln Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr
195 200 205

Gln Gly Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn
210 215 220

Gln Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
225 230 235 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser Gly

245 250 255

Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly Gly Ser
260 265 270

Ser Ser Gly Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly
275 280 285

Ser Ser Gly Asn Ser Gly Gly Ser Arg Gly Asp Ser Gly Ser Glu Ser
290 295 300

Ser Trp Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser
305 310 315 320

Gly Gly Gly Asn Gly His Lys Pro Gly Gly Gln Gly Ser Ser Trp Gly
325 330 335

Ser Gly Gly Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu
340 345 350

Thr Ser Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys
355 360 365

Ser Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asn Gln Val
370 375 380

Pro Pro Pro Ser Thr Arg Ala Leu Leu Tyr Phe Ser Arg Leu Trp Glu
385 390 395 400

Asp Phe Lys Gln Asn Thr Pro Phe Leu Asn Trp Lys Ala Ile Ile Glu
405 410 415

Gly Ala Asp Ala Ser Ser Leu Gln Lys Arg Ala Gly Arg Ala Asp Gln
420 425 430

Asn Tyr Asn Tyr Asn Gln His Ala Tyr Pro Thr Ala Tyr Gly Gly Lys
435 440 445

Tyr Ser Val Lys Thr Pro Ala Lys Gly Gly Val Ser Pro Ser Ser Ser
450 455 460

Ala Ser Arg Val Gln Pro Gly Leu Leu Gln Trp Val Lys Phe Trp
465 470 475

<210> 55
<211> 1532
<212> DNA
<213> Homo sapiens

<400> 55
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gcttccgggt gactgcttcc tactgctcgt gctgctgctc tacgcgccag tcgggttctg 180
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1532

<210> 56
<211> 410
<212> PRT
<213> Homo sapiens

<400> 56
Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
1 5 10 15

Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
20 25 30

Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
35 40 45

Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
50 55 60

Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
65 70 75 80

Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
85 90 95

Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
100 105 110

Thr Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg Gly
115 120 125

Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys Arg
130 135 140

Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro
145 150 155 160

Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser
165 170 175

Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu Gln Val
180 185 190

```
Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp Val Ser
        195                 200                 205

Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln Val Arg
    210                 215                 220

Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe
225                 230                 235                 240

Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu Leu Gly Gln Thr Gly
                245                 250                 255

Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His Met Lys Arg Gln Arg
            260                 265                 270

His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser
        275                 280                 285

Pro Gly Pro Ser Pro Asp Val Gln Leu Ala Thr Leu Ala Gln Arg Val
    290                 295                 300

Lys Glu Val Leu Pro His Val Pro Leu Gly Val Ile Gln Arg Asp Leu
305                 310                 315                 320

Ala Lys Thr Gly Cys Val Asp Leu Thr Ile Thr Asn Leu Leu Glu Gly
                325                 330                 335

Ala Val Ala Phe Met Pro Glu Asp Ile Thr Lys Gly Thr Gln Ser Leu
            340                 345                 350

Pro Thr Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly Pro Val Thr Pro
        355                 360                 365

Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp Ala Arg Gln Glu
    370                 375                 380

Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr Ala Arg Arg Arg
385                 390                 395                 400

Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp
                405                 410
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<210> 57
<211> 2093
<212> DNA
<213> Homo sapiens

<400> 57
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tagtggccct tatcctcctc cactcagcat tggcccagtc ccgtcgagac tttgcaccac 180
caggccaaca gaagagagaa gccccagttg atgtcttgac ccagataggt cgatctgtgc 240
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tcactggctc ccgagcctct ggggcccaac tcgaggccaa ggtgcgaggg ctggaacgcc 720
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aagaataaat gcccaattct tactgttcag gtttgatgtg gaatcacagc tgcagtgata 1980
tatatttttt atcagtgctt ggttggtttt aaataaagtg cacgctattt tattatcttg 2040
ttctgaataa aatgtattta ctccaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2093

<210> 58
<211> 243
<212> PRT
<213> Homo sapiens

<400> 58
Met Ala Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His Val Phe Lys
1 5 10 15

Ala Ile Leu Met Val Leu Val Ala Leu Ile Leu Leu His Ser Ala Leu
20 25 30

Ala Gln Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln Lys Arg Glu
35 40 45

Ala Pro Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val Arg Gly Thr
50 55 60

Leu Asp Ala Trp Ile Gly Pro Glu Thr Met His Leu Val Ser Glu Ser
65 70 75 80

Ser Ser Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser Val Ala Phe
85 90 95

Phe Ala Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala Leu Gly Leu
100 105 110

Ala Gly Asp Tyr Leu Ala Gln Gly Leu Lys Leu Ser Pro Gly Gln Val
115 120 125

Gln Thr Phe Leu Leu Trp Gly Ala Gly Ala Leu Val Val Tyr Trp Leu
130 135 140

Leu Ser Leu Leu Leu Gly Leu Val Leu Ala Leu Leu Gly Arg Ile Leu
145 150 155 160

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Trp Gly Leu Lys Leu Val Ile Phe Leu Ala Gly Phe Val Ala Leu Met
                165                 170                 175

Arg Ser Val Pro Asp Pro Ser Thr Arg Ala Leu Leu Leu Leu Ala Leu
            180                 185                 190

Leu Ile Leu Tyr Ala Leu Leu Ser Arg Leu Thr Gly Ser Arg Ala Ser
        195                 200                 205

Gly Ala Gln Leu Glu Ala Lys Val Arg Gly Leu Glu Arg Gln Val Glu
    210                 215                 220

Glu Leu Arg Trp Arg Gln Arg Arg Ala Ala Lys Gly Ala Arg Ser Val
225                 230                 235                 240

Glu Glu Glu
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<210> 59
<211> 1372
<212> DNA
<213> Homo sapiens

<400> 59
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gccatgtcgg acctgctact actgggcctg attgggggcc tgactctctt actgctgctg 120
acgctgctgg cctttgccgg gtactcaggg ctactggctg gggtggaagt gagtgctggg 180
tcaccccca tccgcaacgt cactgtggcc tacaagttcc acatggggct ctatggtgag 240
actgggcggc ttttcactga gagctgcagc atctctccca agctccgctc catcgctgtc 300
tactatgaca acccccacat ggtgccccct gataagtgcc gatgtgccgt gggcagcatc 360
ctgagtgaag gtgaggaatc gccctccccc gagctcatcg acctctacca gaaatttggc 420
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accattctgt ccatctggct ggctacccgc cgtgtccatc ctgccttgga cacctacatc 540
aaggagcgga agctgtgtgc ctatcctcgg ctggagatct accaggaaga ccagatccat 600
ttcatgtgcc cactggcacg gcagggagac ttctatgtgc ctgagatgaa ggagacagag 660
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acaatgagtg acacgagttc tgtaagcttg gaagtgagcc ctggcagccg ggagacttca 780
gctgccacac tgtcacctgg ggcgagcagc cgtggctggg atgacggtga cacccgcagc 840
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attttctgca ccagccccca gggctgccgc ccctgttgtg tctttttttc agactcacag 1260
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1372

<210> 60
<211> 313
<212> PRT
<213> Homo sapiens

<400> 60
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Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu Thr Leu Leu
  1               5                  10                  15

Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly Leu Leu Ala
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            20                  25                  30

Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn Val Thr Val
         35                  40                  45

Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly Arg Leu Phe
     50                  55                  60

Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile Ala Val Tyr
 65                  70                  75                  80

Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys Ala Val
                 85                  90                  95

Gly Ser Ile Leu Ser Glu Gly Glu Glu Ser Pro Ser Pro Glu Leu Ile
            100                 105                 110

Asp Leu Tyr Gln Lys Phe Gly Phe Lys Val Phe Ser Phe Pro Ala Pro
        115                 120                 125

Ser His Val Val Thr Ala Thr Phe Pro Tyr Thr Thr Ile Leu Ser Ile
    130                 135                 140

Trp Leu Ala Thr Arg Arg Val His Pro Ala Leu Asp Thr Tyr Ile Lys
145                 150                 155                 160

Glu Arg Lys Leu Cys Ala Tyr Pro Arg Leu Glu Ile Tyr Gln Glu Asp
                165                 170                 175

Gln Ile His Phe Met Cys Pro Leu Ala Arg Gln Gly Asp Phe Tyr Val
            180                 185                 190

Pro Glu Met Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val Glu Ala
        195                 200                 205

Ile Asp Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser Asp Thr
    210                 215                 220

Ser Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr Ser Ala
225                 230                 235                 240

Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp Gly Asp
                245                 250                 255

Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly Ser Ser
            260                 265                 270

Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly Glu Ser Arg
        275                 280                 285

Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys Trp Leu Trp Glu
    290                 295                 300

Pro Thr Ala Pro Glu Lys Gly Lys Glu
305                 310
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<210> 61
<211> 1529
<212> DNA

<213> Homo sapiens

<400> 61
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accagcctct ccgtgagtgt tagaaatcac agatacagta tatacttaat tacactaaat 120
tattgctggg attccttata agcactaatt atacctgatt ataggttaaa atatttattt 180
tgtcaaaata ttttcttggg aatgtgttta acccttttctg cgttcattgt tgctgagatg 240
tgaaaactaa ccattccctc ctgcctacct ttttggccac tgggcggcag agaatggcgc 300
tatgtgcagt tgggcccctg gcaccatggg cctttggcct gcctgctgca gagtagccct 360
gcctgggcag tctccaggca ctgagcaggc catctgtggc caggctgaga gaatgactgg 420
ctcgcttacc agcgtgcatg ggacaaggag ctttggagcc tcaaggggtt gttgctggcc 480
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gtgagtgatg gtgccttggt tcactagcct tcccccacca ccccaccatg ccacctggtg 600
gtcttggggc ctgtgctgtc actccagccc ctggggagga gaggacccag cccggagagt 660
tggggcaagg gctccacatg gcccaagggc aacagatgct cgcagggcag ctgctgccga 720
tgctcacgct cctgcccccc tccttcccgc tgccacaccc caccctgggc ccccgcagac 780
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ttgcagcctg gcttcagcct ctggcactgc tggagtggtc cctgggagct tctgcactgt 960
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gtcaccagcc cttcctatct gtggggtcca agtcaggctt cccctgcggc caccagccat 1140
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tcccggagag ggggacggat atttatttcc taaagtttgc acttaattgt gaggattctc 1260
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gagggtgggt cagtgcaccc gaggctcaga gcatccatcc accccactgg ccctccttcc 1440
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gaacaaaaaa aaaaaaaaaa aaaaaaaaa 1529

<210> 62
<211> 136
<212> PRT
<213> Homo sapiens

<400> 62
Met Pro Pro Gly Gly Leu Gly Ala Cys Ala Val Thr Pro Ala Pro Gly
1 5 10 15

Glu Glu Arg Thr Gln Pro Gly Glu Leu Gly Gln Gly Leu His Met Ala
20 25 30

Gln Gly Gln Gln Met Leu Ala Gly Gln Leu Leu Pro Met Leu Thr Leu
35 40 45

Leu Pro Pro Ser Phe Pro Leu Pro His Pro Thr Leu Gly Pro Arg Arg
50 55 60

His Ala Ser Leu Thr Gln Leu Gly Pro Ala Phe Trp Met Ala Trp Gly
65 70 75 80

Arg Pro Trp Ala His Leu Gly Pro Gly Gln Pro Leu Gly Gln Leu Trp
85 90 95

Lys Ser Ser Val Glu Glu His Leu Leu Ala Ala Trp Leu Gln Pro Leu
100 105 110

Ala Leu Leu Glu Trp Ser Leu Gly Ala Ser Ala Leu Ser Ala Leu Gly
115 120 125

Thr Ser His Pro Leu Gly Leu Gln
130 135

<210> 63
<211> 2242
<212> DNA
<213> Homo sapiens

<400> 63
gagctgaggt ggcagtggtt ccaccaacat ggagctctcg cagatgtcgg agctcatggg 60
gctgtcggtg ttgcttgggc tgctggccct gatggcgacg gcggcggtag cgcgggggtg 120
gctgcgcgcg ggggaggaga ggagcggccg gcccgcctgc caaaaagcaa atggatttcc 180
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Gly Phe Pro Pro Asp Lys Ser Ser Gly Ser Lys Lys Gln Lys Gln Tyr
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Gln Arg Ile Arg Lys Glu Lys Pro Gln Gln His Asn Phe Thr His Arg
 65                  70                  75                  80

Leu Leu Ala Ala Ala Leu Lys Ser His Ser Gly Asn Ile Ser Cys Met
                 85                  90                  95

Asp Phe Ser Ser Asn Gly Lys Tyr Leu Ala Thr Cys Ala Asp Asp Arg
            100                 105                 110

Thr Ile Arg Ile Trp Ser Thr Lys Asp Phe Leu Gln Arg Glu His Arg
        115                 120                 125

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    130                 135                 140

Ser Pro Asp Cys Arg Ala Phe Ile Val Trp Leu Ala Asn Gly Asp Thr
145                 150                 155                 160

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Thr Ala Thr Pro Glu Asp Phe Pro Lys Lys His Lys Ala Pro Val Ile
            180                 185                 190

Asp Ile Gly Ile Ala Asn Thr Gly Lys Phe Ile Met Thr Ala Ser Ser
        195                 200                 205

Asp Thr Thr Val Leu Ile Trp Ser Leu Lys Gly Gln Val Leu Ser Thr
    210                 215                 220

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225                 230                 235                 240

Gly Arg Phe Val Ala Ser Cys Gly Phe Thr Pro Asp Val Lys Val Trp
                245                 250                 255

Glu Val Cys Phe Gly Lys Lys Gly Glu Phe Gln Glu Val Val Arg Ala
            260                 265                 270

Phe Glu Leu Lys Gly His Ser Ala Ala Val His Ser Phe Ala Phe Ser
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Asn Asp Ser Arg Arg Met Ala Ser Val Ser Lys Asp Gly Thr Trp Lys
    290                 295                 300

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Leu Lys Thr Gly Arg Phe Glu Glu Ala Ala Gly Ala Ala Pro Cys Arg
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35 40 45

His Ser Ala Glu Glu Ile Gly Ile Ile Ala Gly Lys Arg Ile His Arg
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35 40 45

Ala Asn Ser Leu Cys Glu Pro Arg Thr Pro Asp Pro Lys Pro Ile Asn
50 55 60

Gly Lys Gly Asp Met Gly Val Pro Ser Gln Glu Thr Pro Val Pro Phe
65 70 75 80

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85 90 95

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Ser Asp Val Gln Gly Val Ala Thr Glu Lys Pro Leu Ser Ser Ser Val
        115                 120                 125

Cys Arg Gly Val Trp Pro Cys Gly Leu Gly Gly Ala Val Ile Leu Pro
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<213> Homo sapiens

<400> 99

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Ser Cys Ser Leu Thr Trp Glu Thr Pro Arg Trp Tyr Met Ala Gly Arg
         35                  40                  45

Val Ala Thr Ser Thr Ser Gly Cys His Cys Trp Met Ser Arg Arg Asp
     50                  55                  60

Leu Thr Pro Leu Pro His Pro Ser Glu Pro Gly Val Leu Asp Cys Leu
 65                  70                  75                  80

Gly Pro Cys His Leu Leu Pro Leu Leu Ser Pro Gly Ser Pro Cys Trp
                 85                  90                  95

Val Leu Gly Leu His Phe Ser Leu His Pro Pro Ser Ala Ala Ser Ala
            100                 105                 110

Ser His Ala Leu Thr Ile Thr Ser Leu Pro Pro Gly Leu Leu Pro Phe
        115                 120                 125

Val Gly Val Glu Leu Thr Ala His Pro Gln Ala Leu Met Gly Arg Gly
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<213> Homo sapiens

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Ile Ile Phe Pro Pro Leu
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Ser Leu Leu Ser Pro Ala Ala Ile Leu Val Arg Leu Val Pro Ala Arg
         35                  40                  45

Glu Arg Cys Pro Gln Val Lys Gly Tyr Ser Gly Thr Trp Glu Lys Ala
     50                  55                  60

Pro Gly Arg Phe Pro Cys Gly Pro Ala Gln His Gly Ser Arg Val Gly
 65                  70                  75                  80

Thr Leu Leu Cys Arg Gln Pro Ser Leu Tyr Ser Ser Gly Phe Leu Arg
                 85                  90                  95

Ala Leu Pro Cys Leu Cys Gln Ala Cys Ala Ala Ser His Pro Thr Ala
            100                 105                 110

Ala Trp Glu Arg Pro Ala Thr Leu Pro Val His Thr Leu Pro Val His
        115                 120                 125

Thr Leu Pro Val His Asn Cys Ser Arg Ala Leu Cys Leu Trp Ala Pro
    130                 135                 140

Asn Pro Ser Ser Cys Ser Thr Phe Val Trp His Gly Asp Leu Cys Phe
145                 150                 155                 160

Phe Ser Trp Cys Leu Cys Val Trp Ala Trp Asp Glu Cys Trp Tyr Ala
                165                 170                 175

Leu Arg Thr Phe Leu Ile Ala Pro Cys Thr Leu Glu His Gly Ala Asp
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20 25 30

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35 40 45

Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr
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Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp
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Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly
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Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp
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115 120 125

Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu
130 135 140

Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala
145 150 155 160

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                165                 170                 175

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser
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Ser Ala Ala Gly Pro Trp Pro Pro Pro Val Pro Ser Pro Thr Trp Thr
        195                 200                 205

Leu Ser Trp His Ser Ser Thr Ser Cys Cys Cys Cys Trp Val Pro Ser
    210                 215                 220

Trp Gly Pro Gly Pro Pro Cys Val Ala Ala Thr Ser Ala Gly Val Ser
225                 230                 235                 240

Met Gly Ser Leu Cys Ser Ser Pro Gln Pro Pro Pro Leu Pro Tyr Gly
                245                 250                 255

Trp Cys Gly Ser Ser Cys Ile Leu Thr Ala Thr Ser Ser Thr Thr Val
            260                 265                 270

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Gly Pro Ser Ser Ser Ser Thr Ser Ser Pro Arg Ser Pro Arg
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Cys Gly Leu Ser Thr Ser His Pro Leu Phe Leu Ile Pro Tyr Leu Ser
             20                  25                  30

Arg Ala Cys Pro Thr Ser Glu Val Leu Gly Phe Arg Val Leu Cys Leu
         35                  40                  45

Pro Leu Pro Val Pro Arg Ser Ser Gln Thr Leu Leu Leu Phe Ile Arg
     50                  55                  60

Ala Val Gly Arg Val Phe Leu Leu Phe Leu Gly Thr Cys Pro Cys Ser
 65                  70                  75                  80

Ser His Cys Pro Pro Cys Leu Ser Leu Ile Gln Met Cys His His Gly
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<210> 105
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<211> 18
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Gly Val

<210> 106
<211> 369
<212> PRT
<213> Homo sapiens

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35 40 45

Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly Gly Ala Ala Gly
50 55 60

Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr Arg Glu Ala Val Gly
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Thr Gly Val Arg Gln Val Pro Gly Phe Gly Val Ala Asp Ala Leu Gly
85 90 95

Asn Arg Val Gly Glu Ala Ala His Ala Leu Gly Asn Thr Gly His Glu
100 105 110

Ile Gly Arg Gln Ala Glu Asp Val Ile Arg His Gly Ala Asp Ala Val
115 120 125

Arg Gly Ser Trp Gln Gly Val Pro Gly His Asn Gly Ala Trp Glu Thr
130 135 140

Ser Gly Gly His Gly Ile Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln
145 150 155 160

Gly Gln Gly Asn Pro Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr
165 170 175

Pro Gly Asn Ser Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro
180 185 190

Trp Gly Gln Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr
195 200 205

Gln Gly Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn
210 215 220

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Gln Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
225                 230                 235                 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser Gly
                245                 250                 255

Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly Gly Ser
            260                 265                 270

Ser Ser Gly Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly
        275                 280                 285

Ser Ser Gly Asn Ser Gly Gly Ser Arg Gly Asp Ser Gly Ser Glu Ser
    290                 295                 300

Ser Trp Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser
305                 310                 315                 320

Gly Gly Gly Asn Gly His Lys Pro Gly Asn Ser Glu Thr Ser Pro Gly
                325                 330                 335

Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser Lys Leu Gly
            340                 345                 350

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Pro
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<212> PRT
<213> Homo sapiens

<400> 107

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Gln Cys Gly Gly Ala Leu Ala Cys Ser Leu Ala Ser Ala Ser Gly Thr
             20                  25                  30

Ala Gly Val Val Pro Gly Ser Phe Cys Thr Val Gly Phe Gly Asp Val
         35                  40                  45

Ser Pro Thr Trp Val Thr Val Gly Leu Pro His Pro Glu Arg Ser Val
     50                  55                  60

Ser Thr Pro Glu Thr Leu Ser Val Ser Pro
 65                  70
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/08504

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/04; C07K 14/435; C12N 1/20; C12P 21/02; A61K 38/00
US CL : 536/23.5; 530/351; 435/252.3, 69.5; 514/2
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.5; 530/351; 435/252.3, 69.5; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database Medline on STN, pir60: Accession No:C434597; reference No:A35796. GERSHON, P. D. and MOSS, B. Early transcription factor subunits are encoded by vaccinia virus late genes. Proc. Natl. Acad. Sci. U.S.A. 1990, Vol. 87, pages 4401-4405. Amino Acids LQVGKGQEV.	9
X	Database Medline on STN, swiss-prot37. Accession No:P49682. LOETSCHER et al. Chemokine receptor specific for IP10 and mig: structure, function, and expression in activated T-lymphocytes. 1996. J. EXP. MED. Vol. 184, pages 963-969. Amino acids: ALYSLLFL.	9

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 08 JULY 1999	Date of mailing of the international search report 30 AUG 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer EILEEN B. O'HARA Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/08504

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Database Medline on STN, EST: Accession No:T35343. ADAMS et al. EST83120 Homo sapiens cDNA 5' end similar to None. Initial assesment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence. Available in database Sept. 6, 1995. 100% sequence match over 297 nucleotide bases, corresponding to nucleotides 156 to 453 of SEQ ID NO:1.	1-11

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Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

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B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

SEQUENCE DATA BASE MPSRCH: GenEmbl, EST, N_Geneseq_34, Issued_Patents_NA, PIR_58, SwissProt_36, STREMBL_8, A_Geneseq_34, Issued_Patents_AA, pir60, SwissProt_37,pir_60, sptrembl19, a-geneseq35, a-issued

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-11, drawn to polynucleotides comprising SEQ ID NO:1, the protein encoded by that polynucleotide comprising SEQ ID NO:2, host cells containing said polynucleotides, a recombinant process for producing protein, and a pharmaceutical composition comprising the protein.
Group II, claims 12 and 13, drawn to a polynucleotide comprising SEQ ID NO: 3 and a protein comprising SEQ ID NO: 4.
Group III, claims 14 and 15, drawn to a polynucleotide comprising SEQ ID NO: 5 and a protein comprising SEQ ID NO: 6.
Group IV, claims 16 and 17, drawn to a polynucleotide comprising SEQ ID NO: 7 and a protein comprising SEQ ID NO.
Group V, claims 18 and 19, drawn to a polynucleotide comprising SEQ ID NO: 9 and a protein comprising SEQ ID NO: 10.
Group VI, claims 20 and 21, drawn to a polynucleotide comprising SEQ ID NO: 11 and a protein comprising SEQ ID NO: 12.
Group VII, claims 22 and 23, drawn to a polynucleotide comprising SEQ ID NO: 13 and a protein comprising SEQ ID NO: 14.
Group VIII, claims 24 and 25, drawn to a polynucleotide comprising SEQ ID NO: 15 and a protein comprising SEQ ID NO: 16.
Group IX, claims 26 and 27, drawn to a polynucleotide comprising SEQ ID NO: 17 and a protein comprising SEQ ID NO: 18.
Group X, claims 28 and 29, drawn to a polynucleotide comprising SEQ ID NO: 19 and a protein comprising SEQ ID NO: 20.
Group XI, claims 30 and 31, drawn to a polynucleotide comprising SEQ ID NO: 21 and a protein comprising SEQ ID NO: 22.
Group XII, claims 32 and 33, drawn to a polynucleotide comprising SEQ ID NO: 23 and a protein comprising SEQ ID NO: 24.
Group XIII, claims 34 and 35, drawn to a polynucleotide comprising SEQ ID NO: 25 and a protein comprising SEQ ID NO: 26.
Group XIV, claims 36 and 37, drawn to a polynucleotide comprising SEQ ID NO: 27 and a protein comprising SEQ ID NO: 28.
Group XV, claims 38 and 39, drawn to a polynucleotide comprising SEQ ID NO: 29 and a protein comprising SEQ ID NO: 30.
Group XVI, claims 40 and 41, drawn to a polynucleotide comprising SEQ ID NO: 31 and a protein comprising SEQ ID NO: 32.
Group XVII, claims 42 and 43, drawn to a polynucleotide comprising SEQ ID NO: 33 and a protein comprising SEQ ID NO: 34.
Group XVIII, claims 44 and 45, drawn to a polynucleotide comprising SEQ ID NO: 35 and a protein comprising SEQ ID NO: 36.
Group XIX, claims 46 and 47, drawn to a polynucleotide comprising SEQ ID NO: 37 and a protein comprising SEQ ID NO: 38.
Group XX, claims 48 and 49, drawn to a polynucleotide comprising SEQ ID NO: 39 and a protein comprising SEQ ID NO: 40.
Group XXI, claims 50 and 51, drawn to a polynucleotide comprising SEQ ID NO: 41 and a protein comprising SEQ ID NO: 42.
Group XXII, claims 52 and 53, drawn to a polynucleotide comprising SEQ ID NO: 43 and a protein comprising SEQ ID NO: 44.
Group XXIII, claims 54 and 55, drawn to a polynucleotide comprising SEQ ID NO: 45 and a protein comprising SEQ ID NO: 46.
Group XXIV, claims 56 and 57, drawn to a polynucleotide comprising SEQ ID NO: 47 and a protein comprising SEQ

ID NO: 48.
Group XXV, claims 58 and 59, drawn to a polynucleotide comprising SEQ ID NO: 49 and a protein comprising SEQ ID NO: 50.
Group XXVI, claims 60 and 61, drawn to a polynucleotide comprising SEQ ID NO: 51 and a protein comprising SEQ ID NO: 52.
Group XXVII, claims 62 and 63, drawn to a polynucleotide comprising SEQ ID NO: 53 and a protein comprising SEQ ID NO: 54.
Group XXVIII, claims 64 and 65, drawn to a polynucleotide comprising SEQ ID NO: 55 and a protein comprising SEQ ID NO: 56.
Group XXIX, claims 66 and 67, drawn to a polynucleotide comprising SEQ ID NO: 57 and a protein comprising SEQ ID NO: 58.
Group XXX, claims 68 and 69, drawn to a polynucleotide comprising SEQ ID NO: 59 and a protein comprising SEQ ID NO: 60.
Group XXXI, claims 70 and 71, drawn to a polynucleotide comprising SEQ ID NO: 61 and a protein comprising SEQ ID NO: 62.
Group XXXII, claims 72 and 73, drawn to a polynucleotide comprising SEQ ID NO: 63 and a protein comprising SEQ ID NO: 64.

The inventions listed as Groups I-XXXII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Pursuant to 37 C.F.R. §.1.475 (b-d), the ISA/US considers that where multiple processes are claimed, the main invention shall consist of the first invention of the category first mentioned in the claims and the first recited invention of each of the other categories related thereto. Accordingly, the main invention (Group I) comprises the first recited product, a polynucleotide comprising SEQ ID NO:1, the polypeptide it encodes comprising SEQ ID NO:2, vectors comprising the polynucleotides, host cells comtaining the polynucleotides and methods of producing the polypeptide. Further pursuant to 37 C.F.R. § 1.475(b-d), the ISA/US considers that any feature which the subsequently recited products and methods share with the main invention does not constitute a special techincal feature within the meaning of PCT Rule 13.2 and that each of such products and methods accordingly defines a separate invention.